



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 01:40 PM UTC

PDB ID : 3J7O / pdb_00003j7o
EMDB ID : EMD-2649
Title : Structure of the mammalian 60S ribosomal subunit
Authors : Voorhees, R.M.; Fernandez, I.S.; Scheres, S.H.W.; Hegde, R.S.
Deposited on : 2014-08-01
Resolution : 3.40 Å(reported)
Based on initial models : 3J3F, 3J3B

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

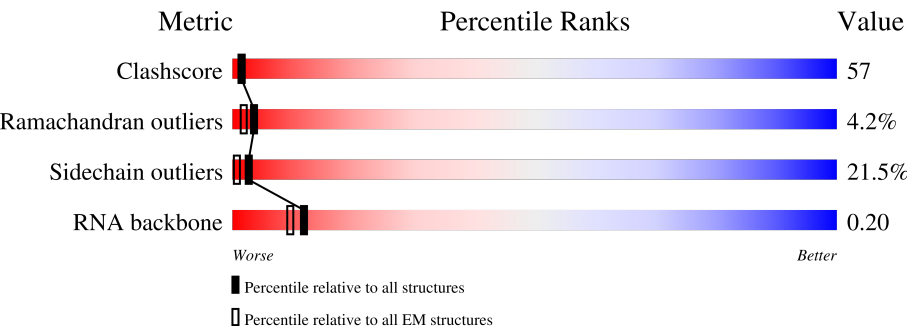
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	5	3664	74% 8% 41% 33% 19%
2	7	120	64% 18% 55% 19% 8%
3	8	156	83% 6% 48% 28% 17%
4	A	257	61% 49% 28% 12% 6% 5%
5	B	394	73% 46% 34% 13% 7%
6	C	367	66% 53% 33% 11% .
7	D	297	64% 43% 36% 14% 5% .

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Mol	Chain	Length	Quality of chain
8	E	236	
9	F	225	
10	G	266	
11	H	192	
12	I	213	
13	J	178	
14	L	211	
15	M	213	
16	N	204	
17	O	204	
18	P	153	
19	Q	188	
20	R	196	
21	S	224	
22	T	160	
23	U	128	
24	V	140	
25	W	157	
26	X	156	
27	Y	145	
28	Z	136	
29	a	148	
30	b	160	
31	c	115	
32	d	125	

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Mol	Chain	Length	Quality of chain
33	e	135	
34	f	110	
35	g	117	
36	h	123	
37	i	105	
38	j	86	
39	k	70	
40	l	51	
41	m	128	
42	n	25	
43	o	106	
44	p	91	
45	r	125	

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 136815 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called Ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 5 is a protein called Ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	394	Total	C	N	O	S	0	0
			3147	2005	591	538	13		

- Molecule 6 is a protein called Ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	367	Total	C	N	O	S	0	0
			2919	1836	582	486	15		

- Molecule 7 is a protein called Ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	292	Total	C	N	O	S	0	0
			2380	1508	434	426	12		

- Molecule 8 is a protein called Ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	236	Total	C	N	O	S	0	0
			1904	1219	364	316	5		

- Molecule 9 is a protein called Ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 10 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	241	Total	C	N	O	S	0	0
			1934	1232	372	326	4		

- Molecule 11 is a protein called Ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called Ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	213	Total	C	N	O	S	0	0
			1713	1083	331	284	15		

- Molecule 13 is a protein called Ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	170	Total	C	N	O	S	0	0
			1359	856	256	241	6		

- Molecule 14 is a protein called Ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	210	Total	C	N	O	S	0	0
			1703	1064	354	280	5		

- Molecule 15 is a protein called Ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	138	Total	C	N	O	S	0	0
			1131	727	216	181	7		

- Molecule 16 is a protein called Ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	201	Total	C	N	O	S	0	0
			1651	1063	323	260	5		

- Molecule 18 is a protein called Ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called Ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 20 is a protein called Ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 21 is a protein called Ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 22 is a protein called Ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 24 is a protein called Ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called Ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 26 is a protein called Ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 27 is a protein called Ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called Ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 29 is a protein called Ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	147	Total	C	N	O	S	0	0
			1163	735	239	185	4		

- Molecule 30 is a protein called Ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 31 is a protein called Ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 32 is a protein called Ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called Ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called Ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called Ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 36 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	122	Total	C	N	O	S	0	0
			1015	642	205	167	1		

- Molecule 37 is a protein called Ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called Ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

- Molecule 39 is a protein called Ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 40 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 43 is a protein called Ribosomal protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 44 is a protein called Ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	125	Total	C	N	O	S	0	0
			1001	622	206	168	5		

- Molecule 46 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
46	5	119	Total	Mg	0
			119	119	
46	7	5	Total	Mg	0
			5	5	
46	8	4	Total	Mg	0
			4	4	
46	P	1	Total	Mg	0
			1	1	
46	V	1	Total	Mg	0
			1	1	

- Molecule 47 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
47	j	1	Total	Zn	0
			1	1	
47	m	1	Total	Zn	0
			1	1	

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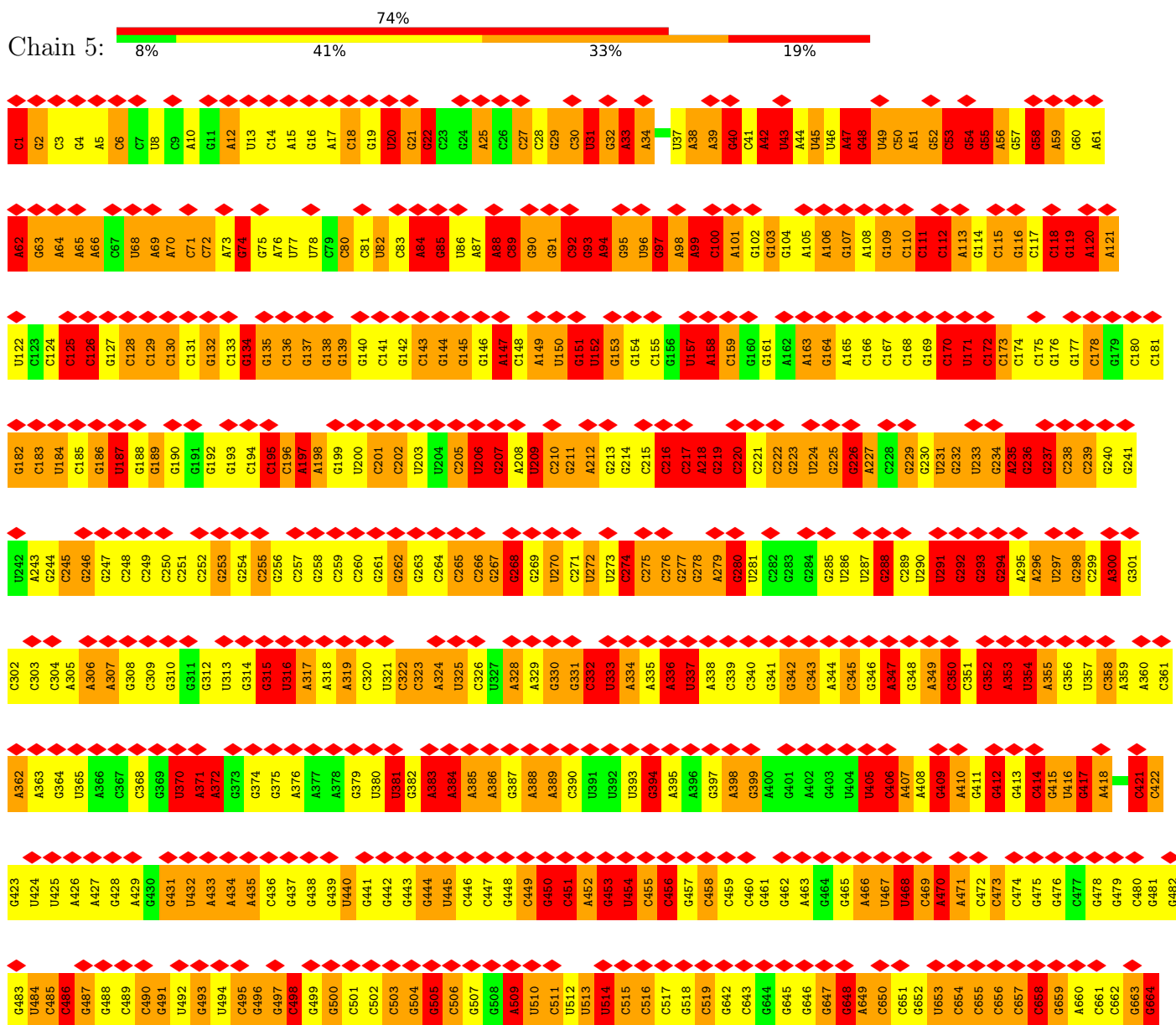
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Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
47	o	1	1	1	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 28S ribosomal RNA



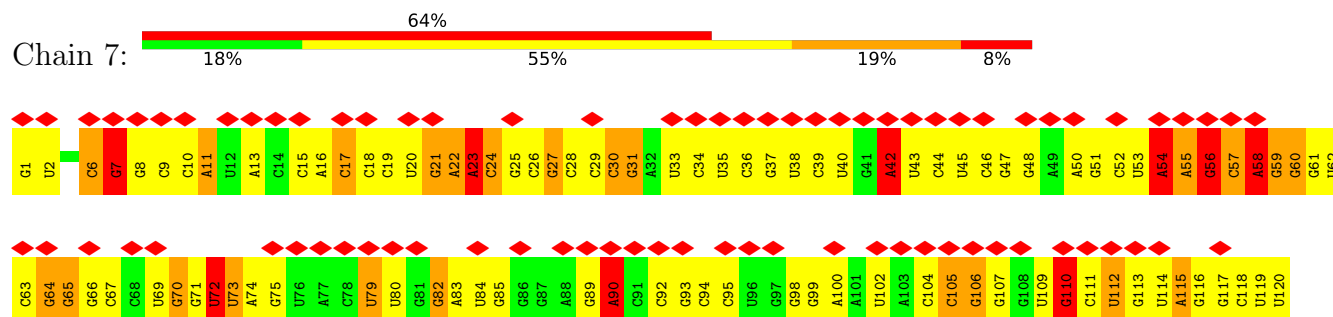
A1669	G1489	C1309	G1249	C1180	G993	G933	G725	C665
G1670	G1490	C1310	C1250	C1181	G994	C834	G726	G666
U1671	A1491	G1311	C1251	C1182	C995	A935	C727	A667
U1672	G1492	A1312	C1252	C1183	G996	C836	U728	C668
U1673	G1493	C1313	C1253	C1184	C997	U937	G729	G669
C1674	U1494	C1314	A1254	G1185	C1047	G938	G730	G670
C1675	G1495	C1315	A1255	U1186	G1048	G939	G731	G671
G1676	G1496	G1316	A1256	G1187	C1049	C940	A732	C672
U1677	A1497	U1317	A1257	G1188	C1050	C941	A733	C673
C1678	G1498	C1318	G1258	C1189	G1051	G942	G734	G674
A1679	C1499	U1319	G1259	G1190	G1064	A943	G735	C675
G1680	U1500	U1320	G1260	C1191	G1065	A944	C736	C676
G1681	C1501	A1321	G1261	C1192	G1066	U945	C737	G677
A1682	G1502	C1323	G1262	C1193	G1067	U946	C738	C678
U1683	A1503	A1324	A1263	G1194	G1068	C947	G739	C679
A1684	G1504	C1325	C1264	G1195	G1069	G948	G740	G680
G1685	C1505	A1326	G1265	G1196	G1070	G949	C741	
C1686	G1506	C1327	G1266	C1197	C1071	G950	G742	G681
U1687	C1507	G1328	C1267	G1198	C1072	G951	G743	G682
G1688	A1508	U1329	G1268	G1199	G1073	G952	G744	C683
G1689	C1509	A1330	G1269	G1200	G1074	C953	G745	G684
C1690	G1510	C1331	A1270	U1201	G1075	C954	A746	C685
A1691	U1511	C1332	C1271	C1202	C1076	G955	A747	A686
C1692	G1512	A1333	G1272	C1203	C1077	U956	G748	U687
U1693	U1513	C1334	G1273	G1204	A1078	A956	G749	U688
A1694	U1514	A1335	A1274	G1205	C1079	G957	U750	U689
C1695	A1515	G1336	G1275	C1206	C1080	C690	G751	C690
U1696	G1516	A1337	A1276	C1207	C1081	G958	G752	C691
C1697	C1517	G1338	G1277	G1208	C1082	A959	C753	A692
A1697	U1518	U1339	C1278	U1209	U1083	G961	C754	C693
U1698	G1519	C1340	A1279	C1210	C1084	C962	C755	C694
C1699	C1520	U1341	C1280	C1211	C1085	G963	G756	G695
A1700	U1521	A1342	G1281	G1212	C1086	A964	G757	C696
U1701	C1522	C1343	C1282	G1213	A1087	G965	C906	G697
C1702	A1523	A1344	G1283	G1214	C1088	A966	C907	G698
A1703	U1524	C1345	C1284	C1215	G1089	C967	G908	G699
U1704	A1525	G1406	U1285	C1216	G1090	C968	A909	G700
C1705	G1526	C1407	G1286	G1217	C1091	C969	G910	G701
U1706	A1527	U1348	C1287	G1218	C1092	G970	U911	U702
A1707	U1528	G1349	G1288	G1219	G1093	G971	G912	G703
C1708	C1529	C1350	C1289	G1220	G1094	C972	G913	C704
U1709	G1530	G1351	G1290	G1221	A1095	C973	U914	G705
A1710	U1531	C1352	G1291	A1222	C1096	C974	A915	C706
C1711	G1532	G1353	C1292	G1232	C1097	C975	C916	C707
U1712	A1533	A1354	G1293	G1233	G1098	C976	A917	G708
A1713	C1534	C1355	A1294	G1234	C977	G978	G918	G709
U1714	G1535	G1356	C1295	G1235	C979	G979	G919	G710
C1715	U1536	C1357	G1296	C1236	C1167	C980	C920	C712
U1716	A1537	G1358	C1297	C1237	G1168	C981	C921	G714
G1717	U1538	U1359	C1298	C1238	G1169	U982	C922	G715
A1718	G1539	G1360	C1299	C1239	G1170	C983	C923	G716
C1719	C1540	C1361	G1300	G1240	G1171	C984	C924	U717
U1720	U1541	G1362	C1301	G1241	C1172	C985	G925	G718
A1721	G1542	C1363	U1302	C1242	G1173	C986	G926	U719
C1722	U1543	G1364	A1303	G1243	G1174	C987	G927	C719
U1723	G1544	C1365	C1304	G1244	A1175	C988	C928	G720
A1724	U1545	G1366	C1305	C1245	C1176	C989	G929	G721
C1725	G1546	C1367	C1306	G1246	U1177	C990	G930	G722
U1726	A1547	A1368	C1307	U1247	G1178	C991	C931	A723
A1727	G1548	U1428	C1308	U1248	U1179	C992	A932	C724



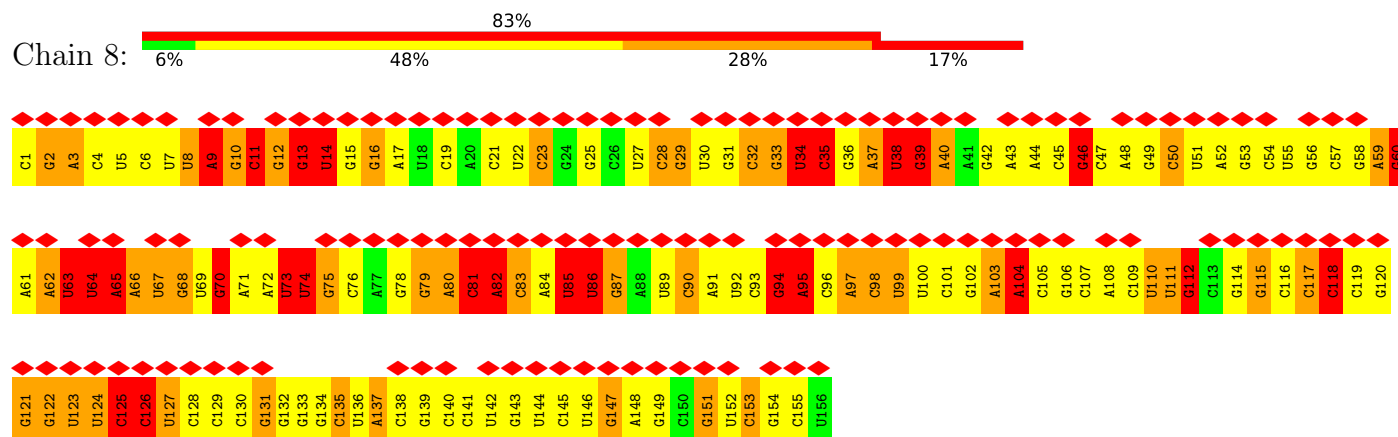
G4150	G4090	C3854	C3794	U3734	G3674	C3614	A2882	G2822	U2761	G2700	G2640
G4151	G4091	C3855	A3795	G3735	G3675	G3615	G2883	G2883	G2762	U2701	A2641
G4152	G4092	A3856	U3796	A3736	G3676	U3616	G2884	C2824	U2763	C2702	A2642
G4153	G4093	G3857	C3797	A3737	U3677	G3617	A2885	A2825	A2764	G2703	G2643
G4154	G4094	G3858	C3798	G3738	U3678	G3618	U2886	U2826	A2765	C2704	G2644
G4155	G4095	G3859	U3799	G3739	U3679	G3619	U2887	G2827	A2766	G2705	G2645
G4156	G4096	A3860	U3799	C3739	U3680	G3620	U2888	U2828	U2767	G2706	G2646
G4157	G4097	A3861	A3800	G3740	G3681	A3621	G2889	U2829	U2769	U2707	A2647
G4158	G3922	A3862	U3801	G3741	A3682	C3622	G2890	G2830	G2770	U2708	G2648
G4159	A3923	C3863	U3802	G3742	C3683	C3623	G2891	G2831	G2771	G2709	G2649
G4160	C3924	C3864	A3803	G3743	G3684	A3624	G2892	C2832	C2772	C2710	G2650
G4161	U3925	A3865	G3804	G3744	C3685	G3625	U2893	A2833	G2773	G2711	C2651
U4162	C3926	C3866	U3805	U3745	G3686	G3626	A2894	C2834	G2774	G2712	C2652
U4163	U3927	A3867	G3806	A3746	G3687	G3627	A2895	A2835	C2775	C2713	C2653
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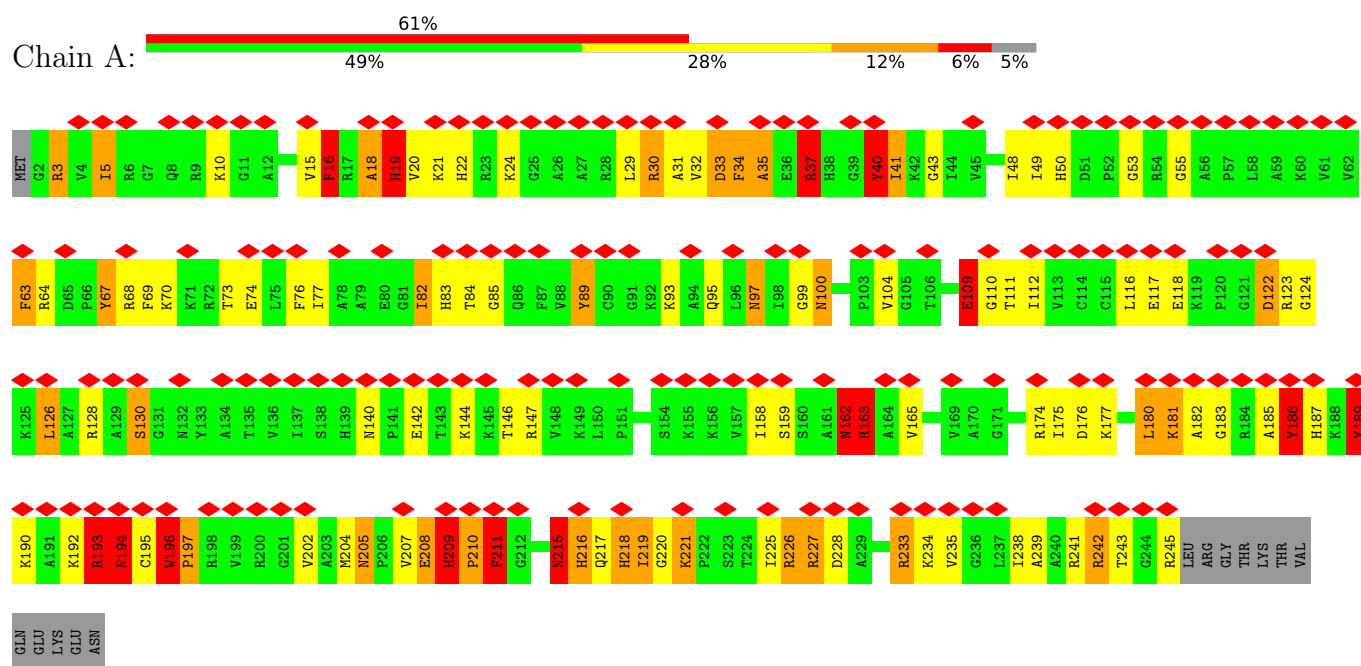
- Molecule 2: 5S ribosomal RNA



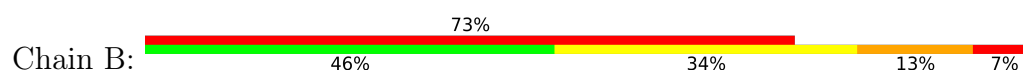
- Molecule 3: 5.8S ribosomal RNA

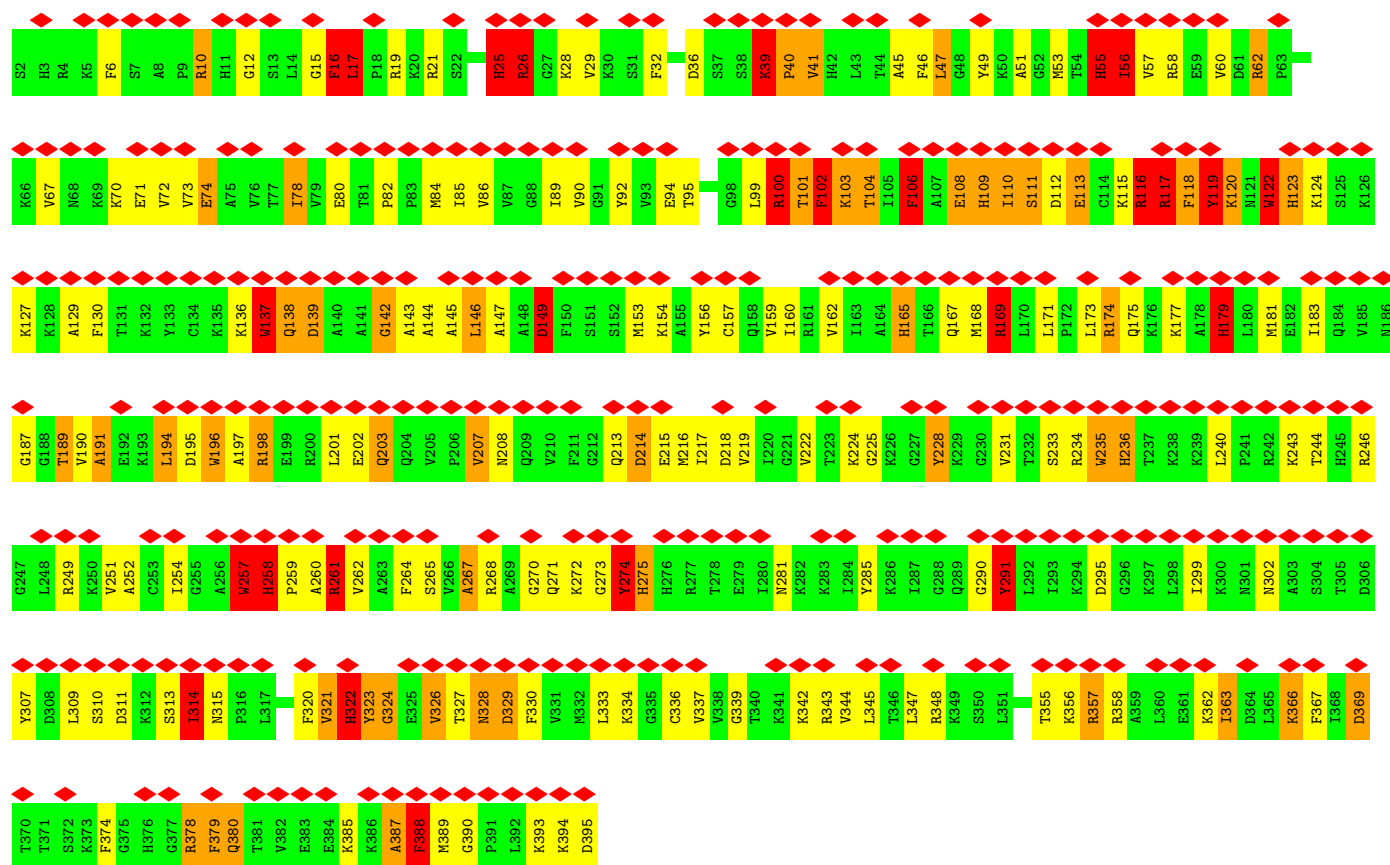


- Molecule 4: Ribosomal protein uL2

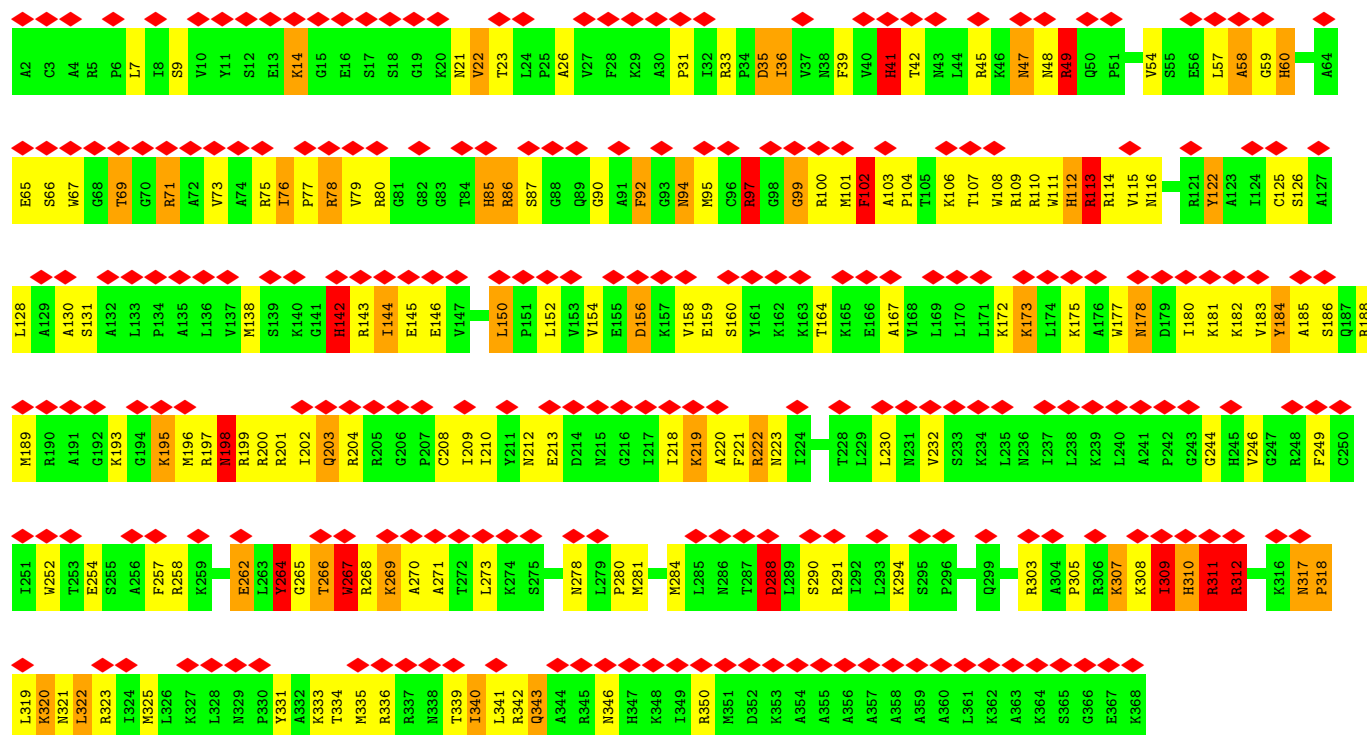


- Molecule 5: Ribosomal protein uL3

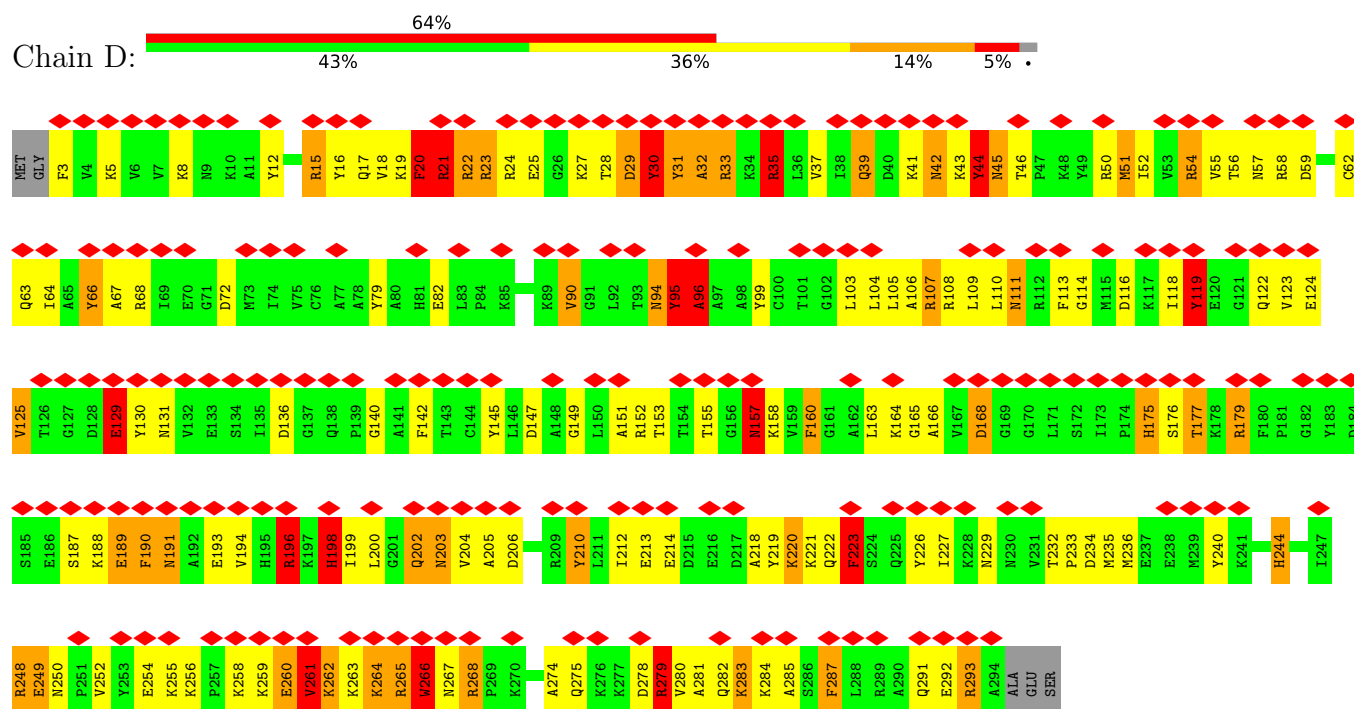




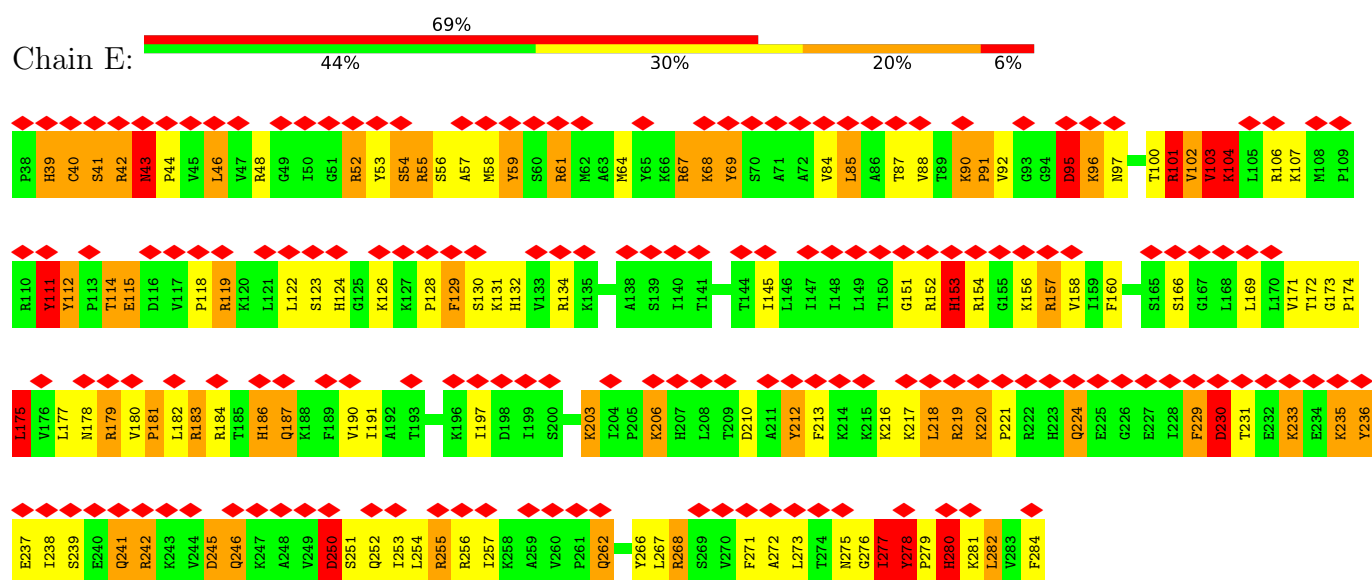
• Molecule 6: Ribosomal protein uL4



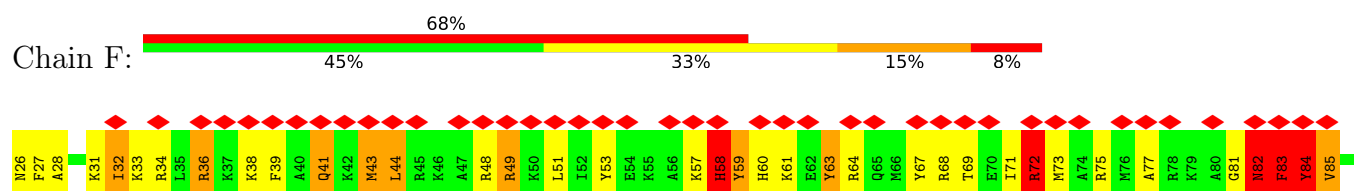
- Molecule 7: Ribosomal protein uL18

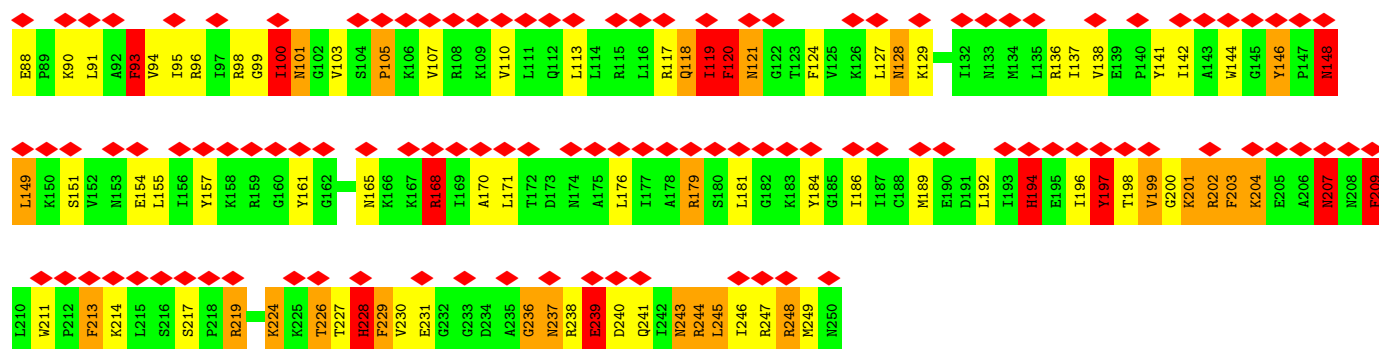


- Molecule 8: Ribosomal protein eL6

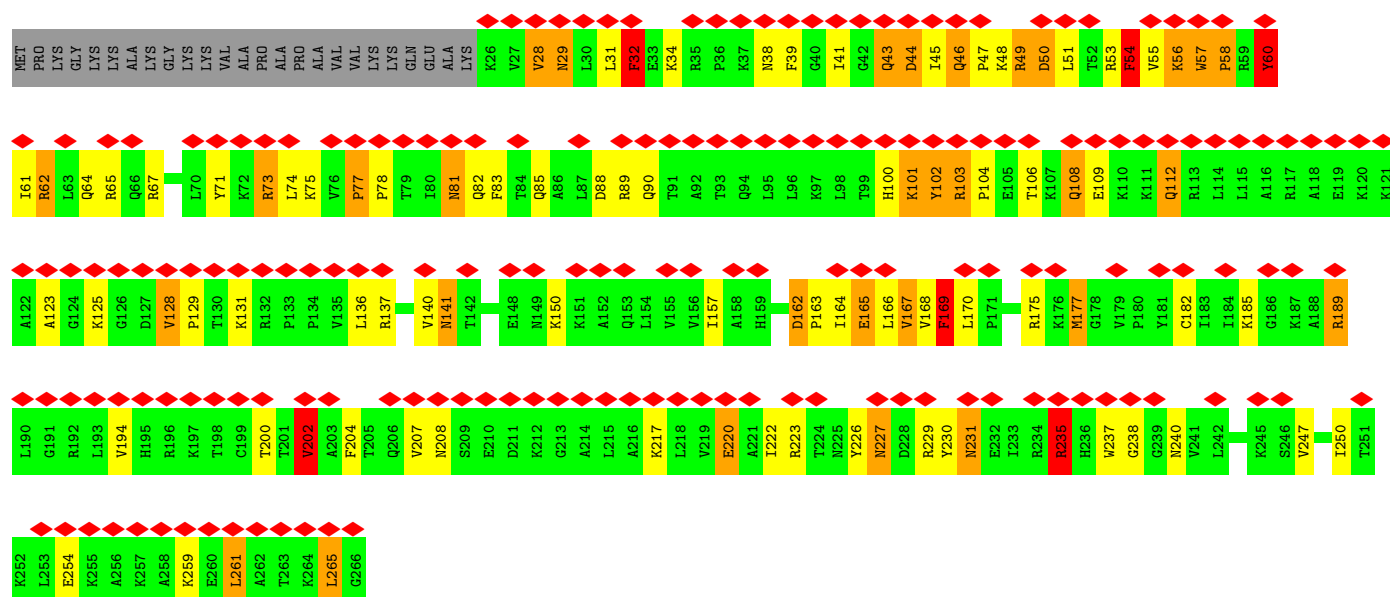


- Molecule 9: Ribosomal protein uL30

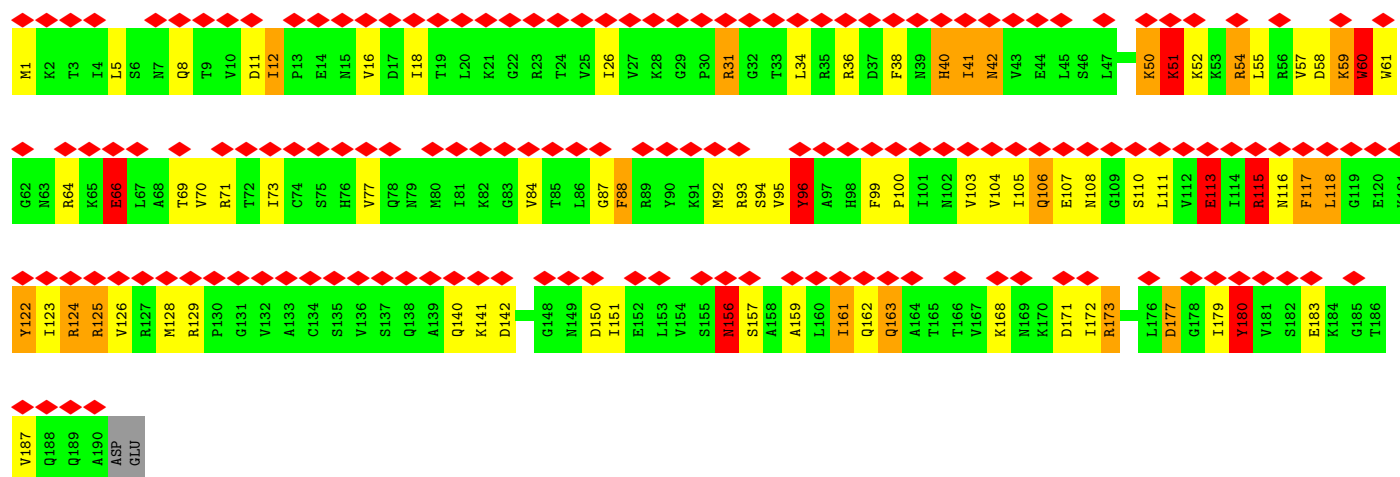
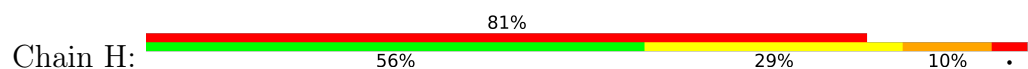




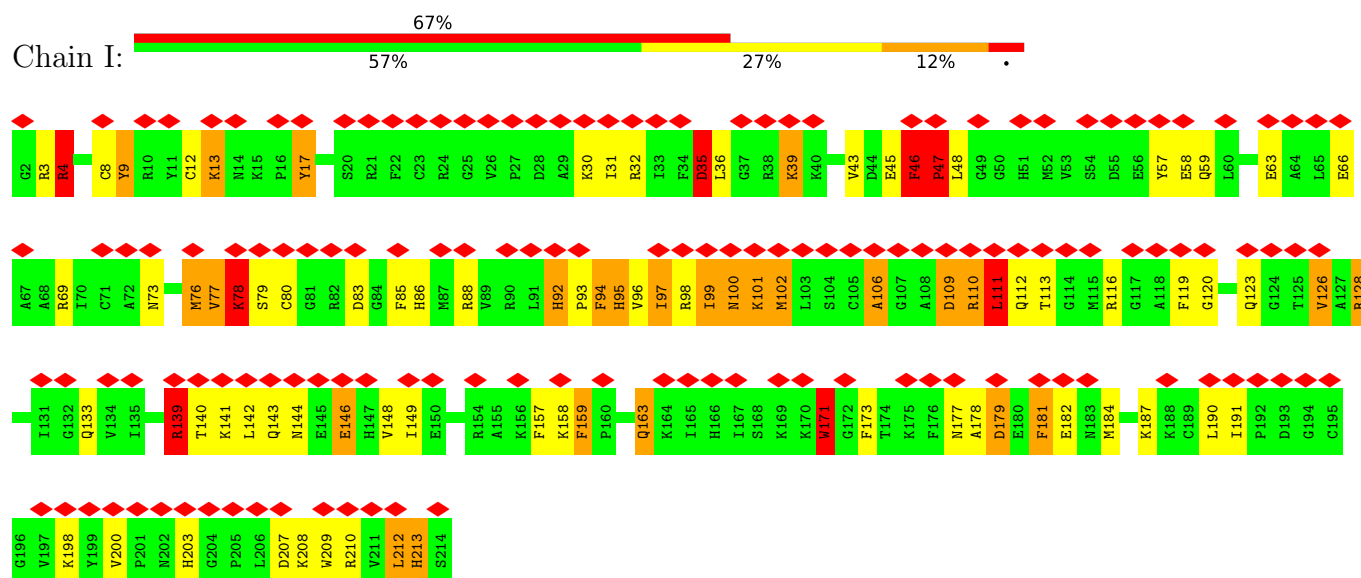
• Molecule 10: Ribosomal protein eL8



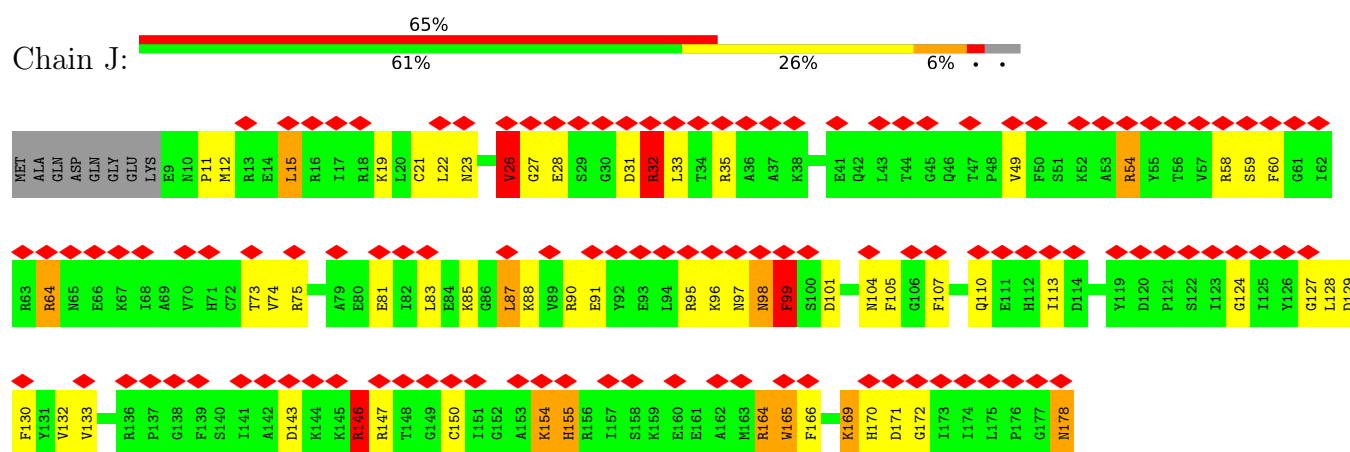
• Molecule 11: Ribosomal protein uL6



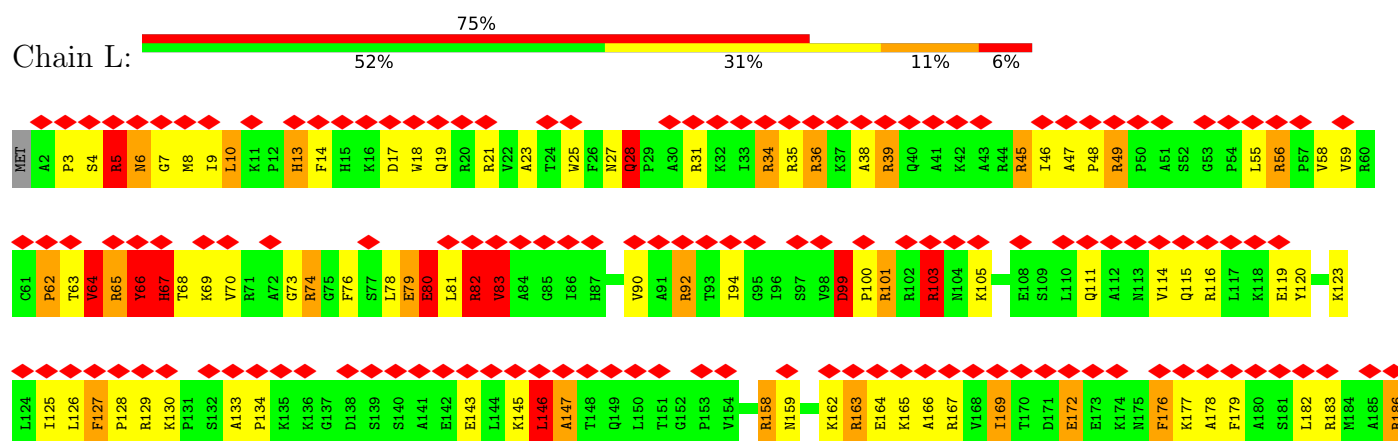
• Molecule 12: Ribosomal protein uL16



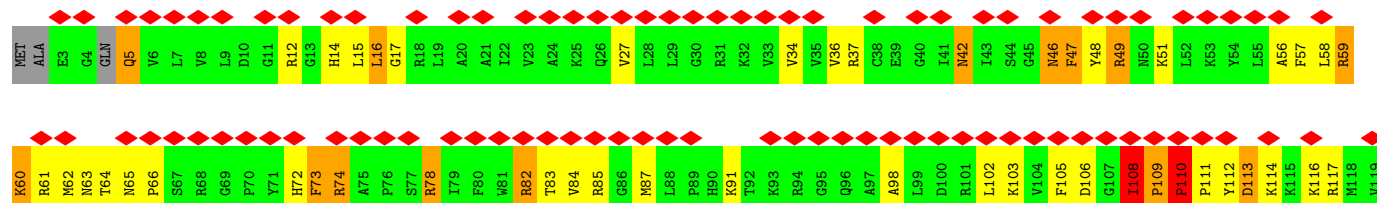
• Molecule 13: Ribosomal protein uL5

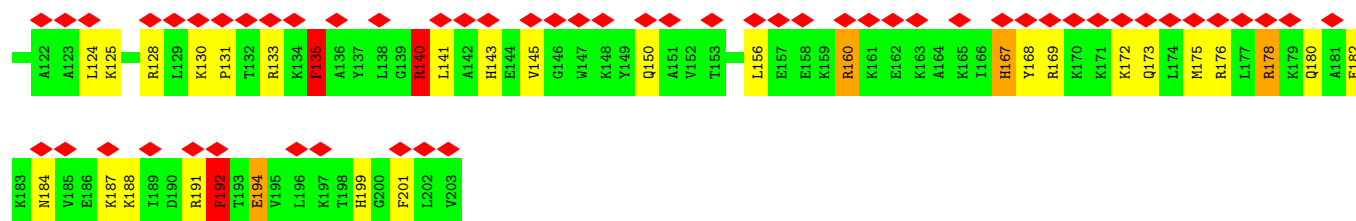


• Molecule 14: Ribosomal protein eL13

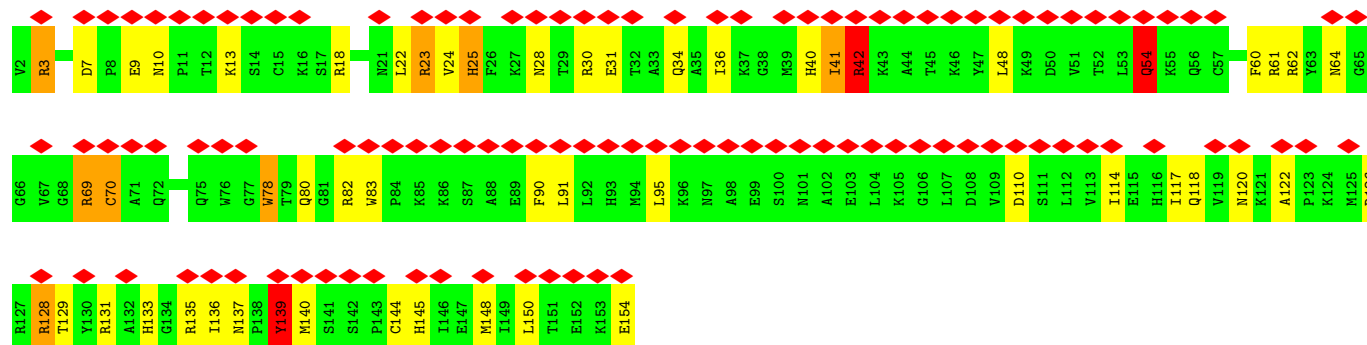
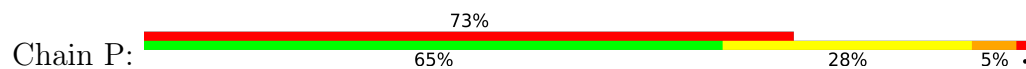


Chain M:

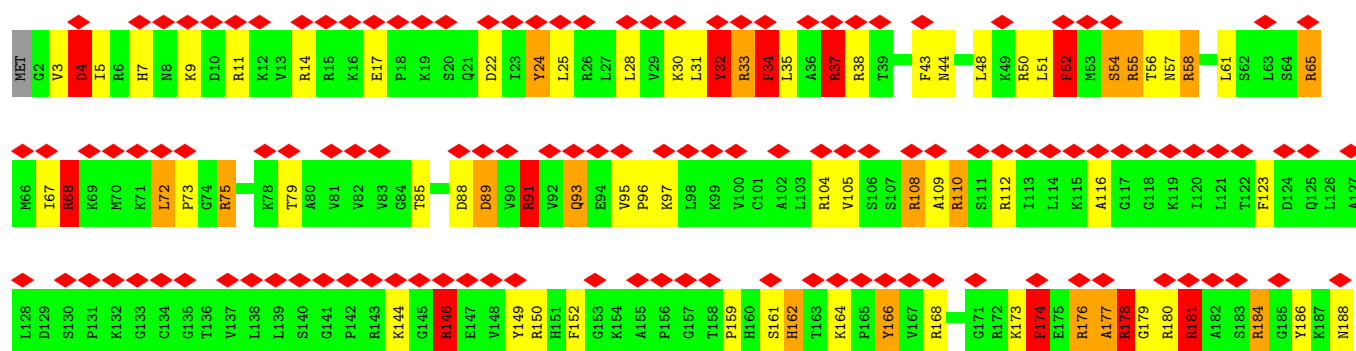




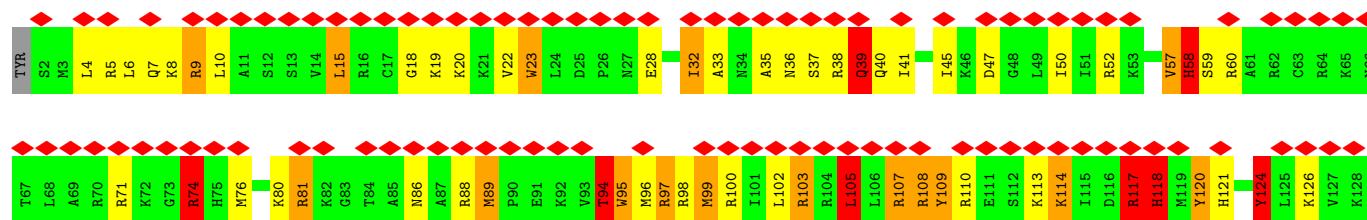
• Molecule 18: Ribosomal protein uL22

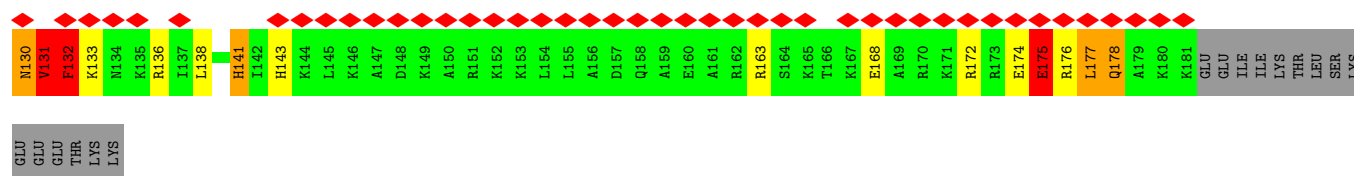


• Molecule 19: Ribosomal protein eL18

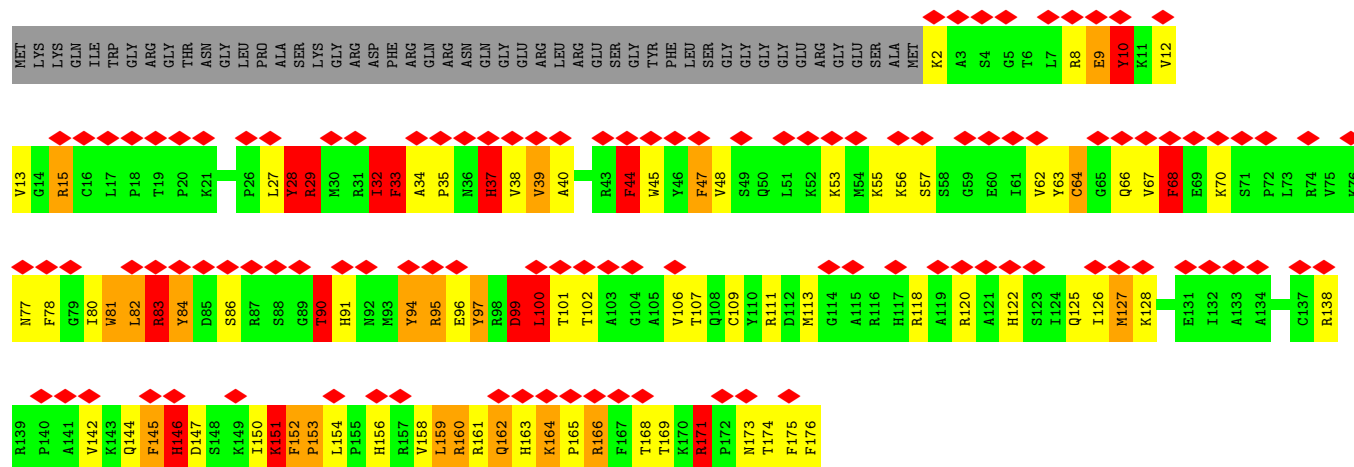


• Molecule 20: Ribosomal protein eL19

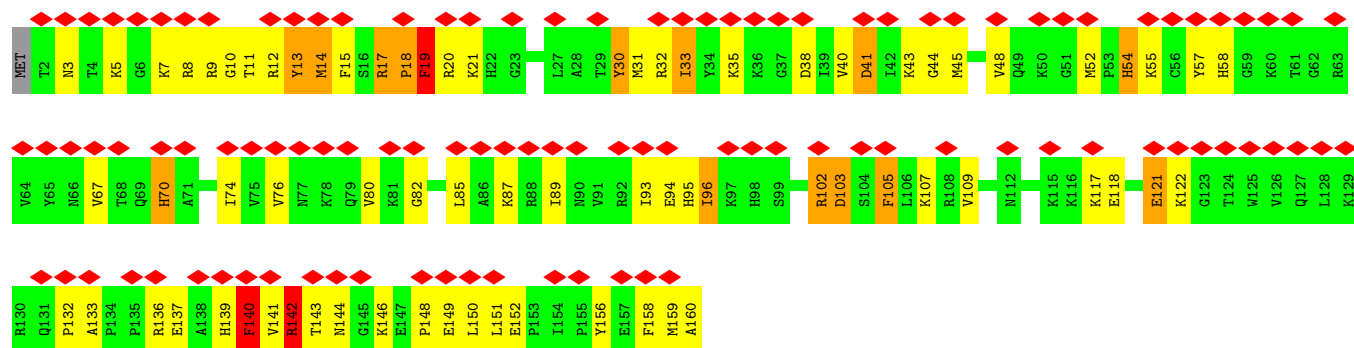




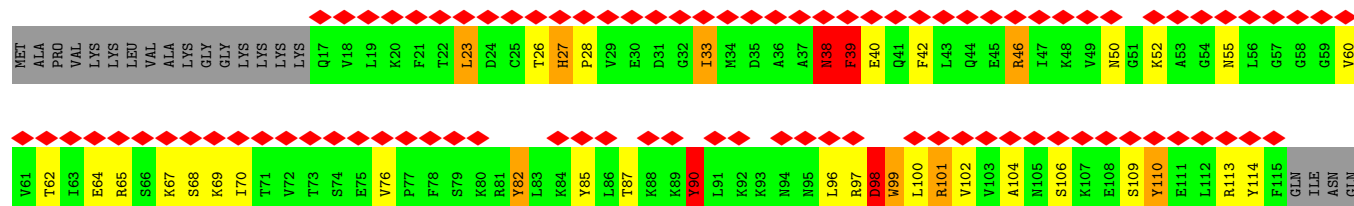
• Molecule 21: Ribosomal protein eL20



• Molecule 22: Ribosomal protein eL21



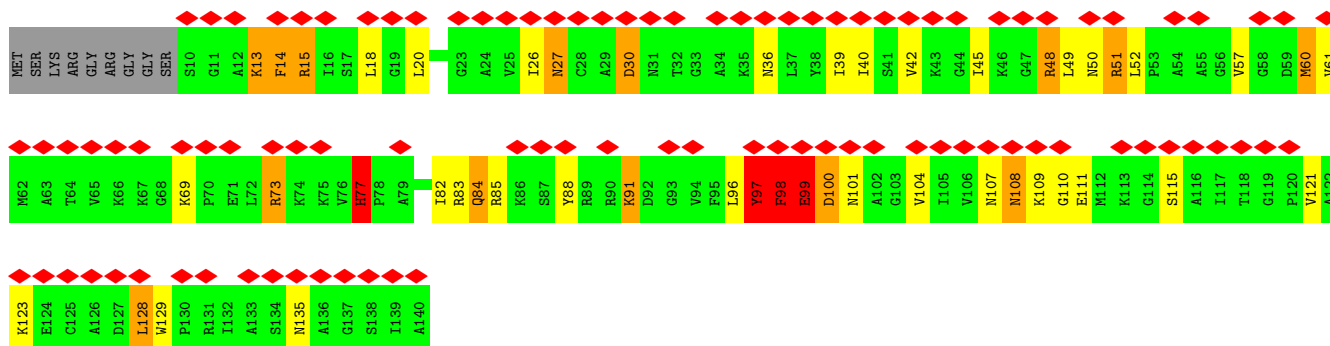
• Molecule 23: Ribosomal protein eL22



GLU
GLU
GLU
GLU
GLU
ASP
ASP

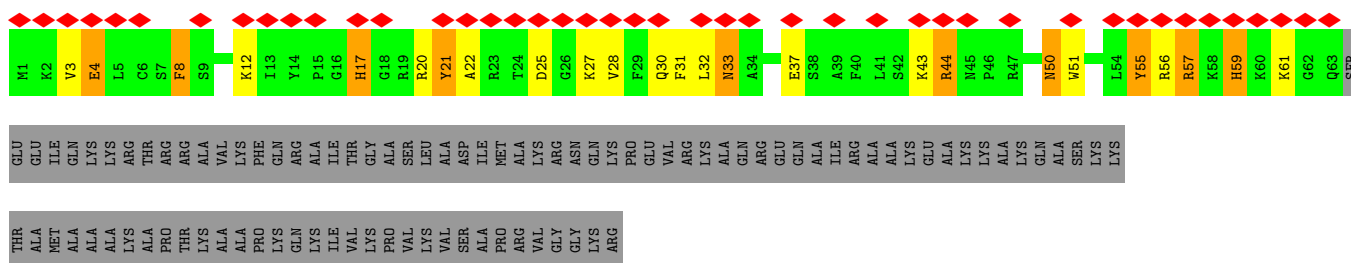
• Molecule 24: Ribosomal protein uL14

Chain V: 



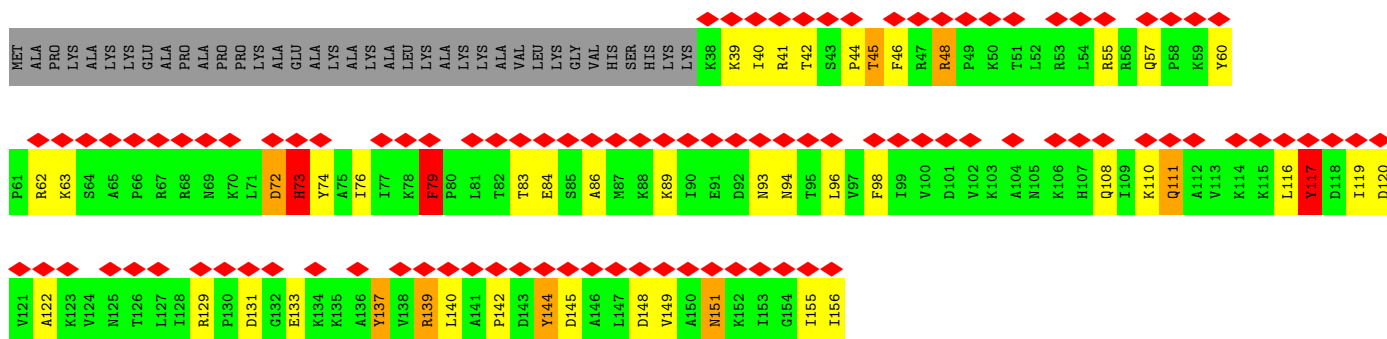
• Molecule 25: Ribosomal protein eL24

Chain W: 



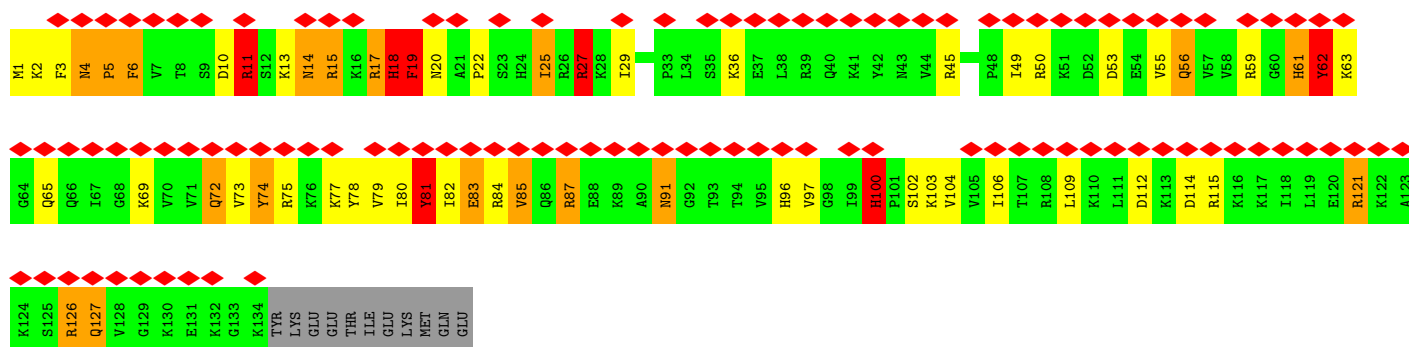
• Molecule 26: Ribosomal protein uL23

Chain X: 

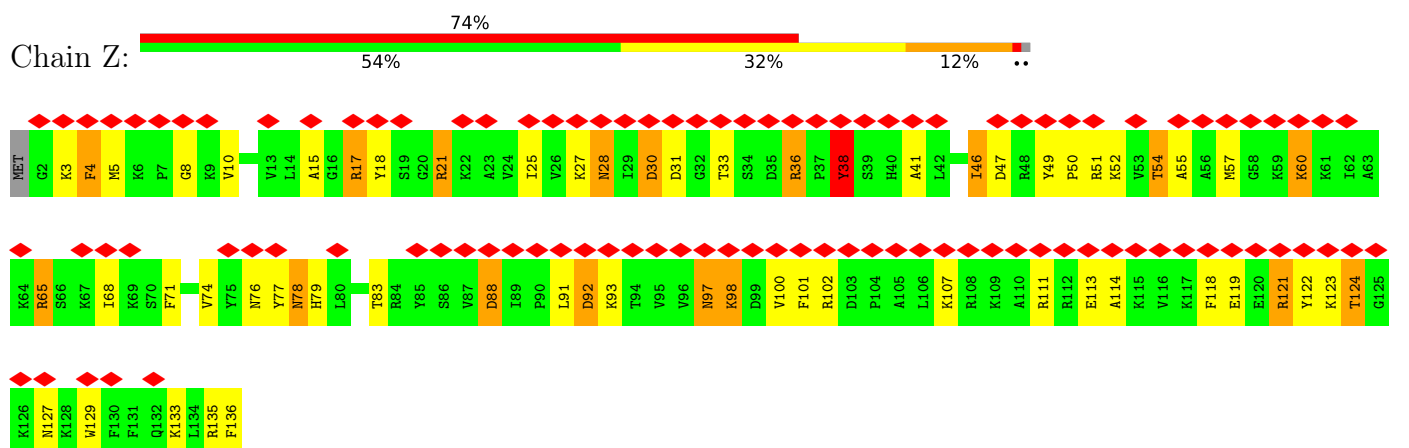


• Molecule 27: Ribosomal protein uL24

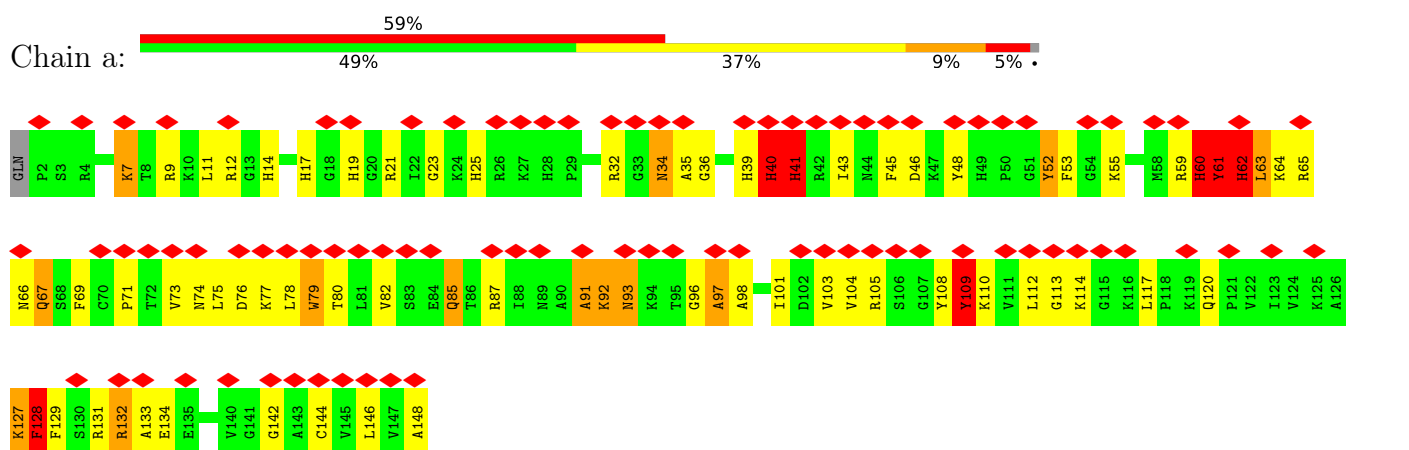
Chain Y: 



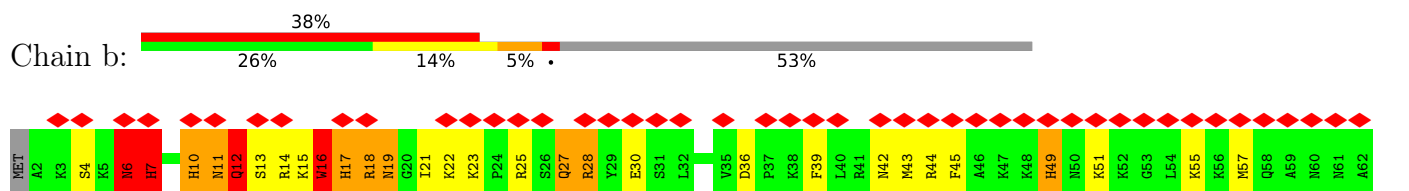
• Molecule 28: Ribosomal protein eL27

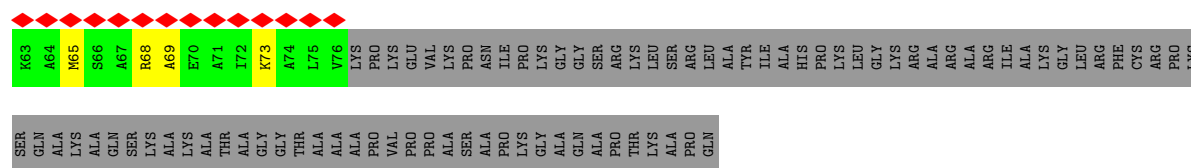


• Molecule 29: Ribosomal protein uL15



• Molecule 30: Ribosomal protein eL29

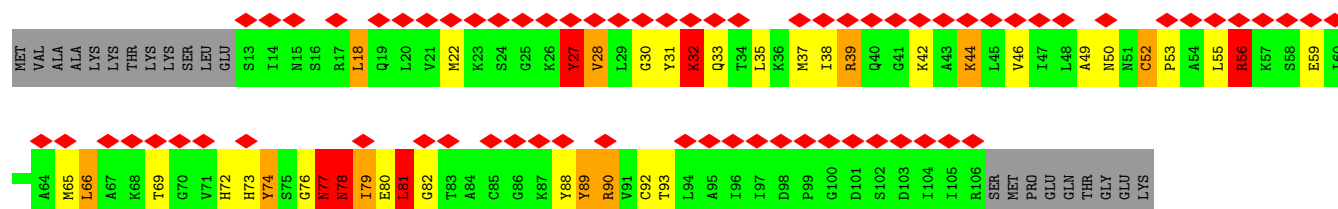




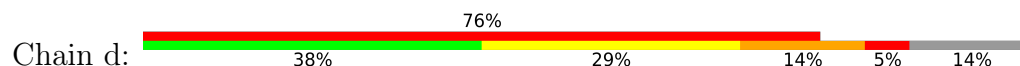
• Molecule 31: Ribosomal protein eL30



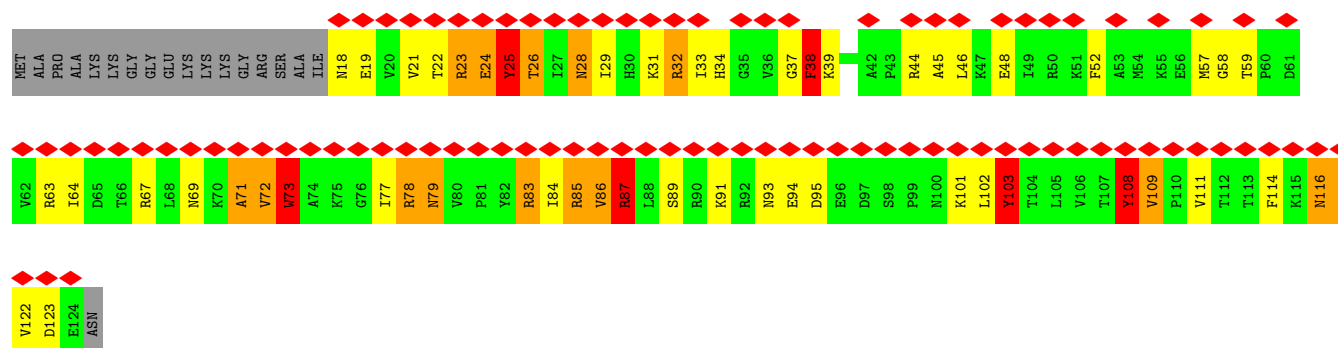
Chain c:



• Molecule 32: Ribosomal protein eL31



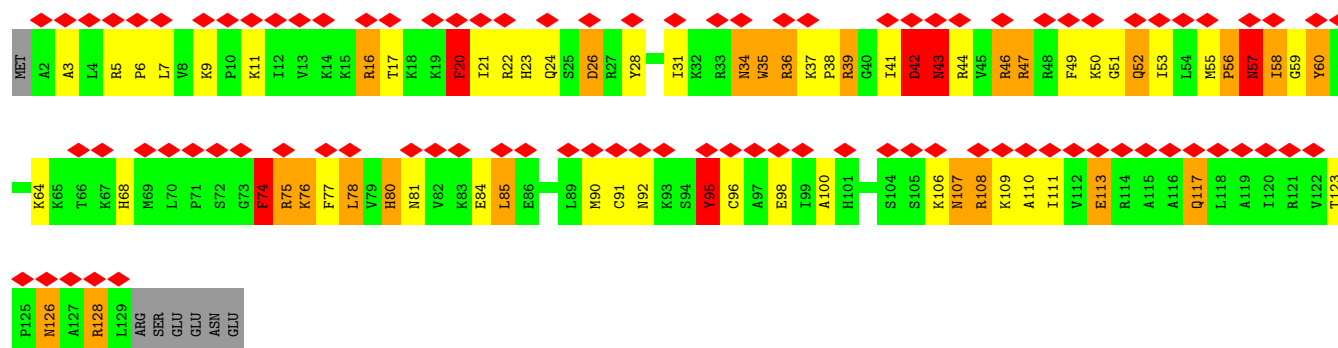
Chain d:



• Molecule 33: Ribosomal protein eL32



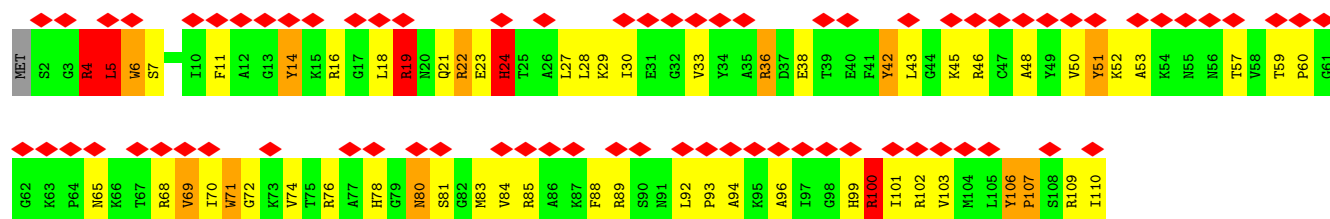
Chain e:



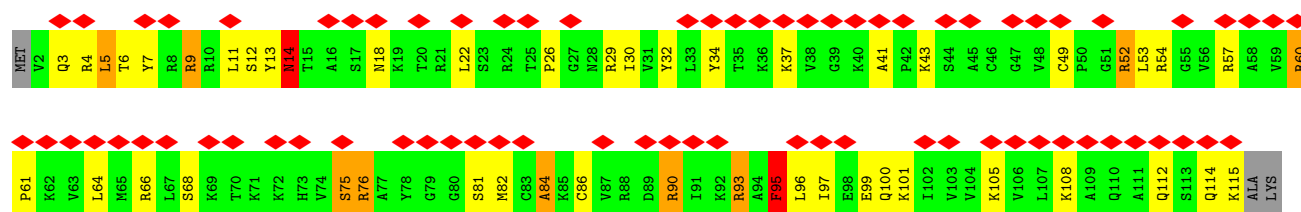
• Molecule 34: Ribosomal protein eL33



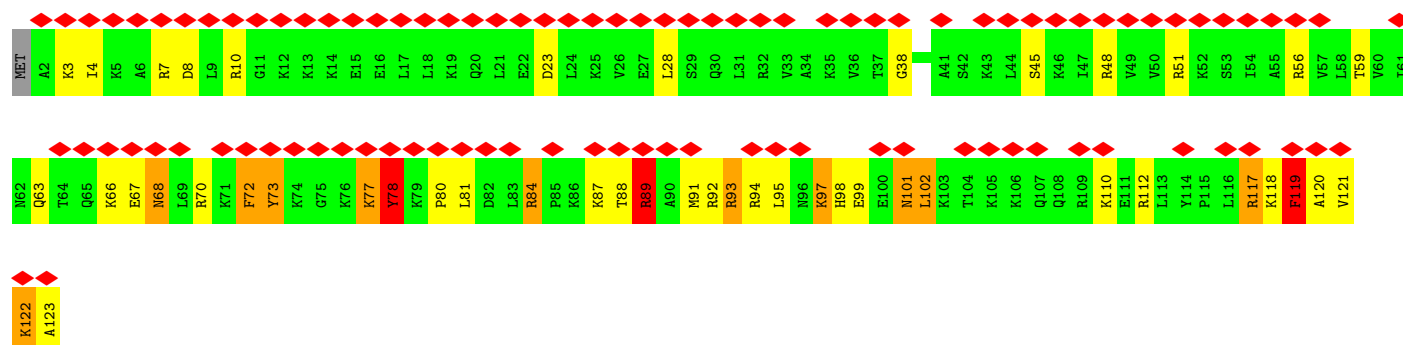
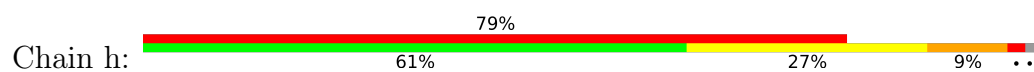
Chain f:



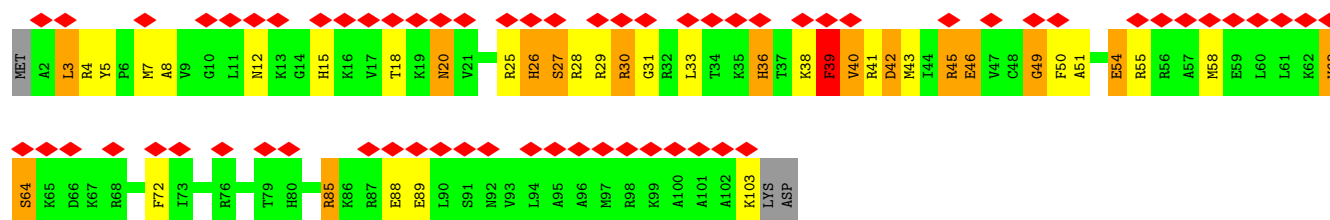
• Molecule 35: Ribosomal protein eL34



• Molecule 36: Ribosomal protein uL29



• Molecule 37: Ribosomal protein eL36

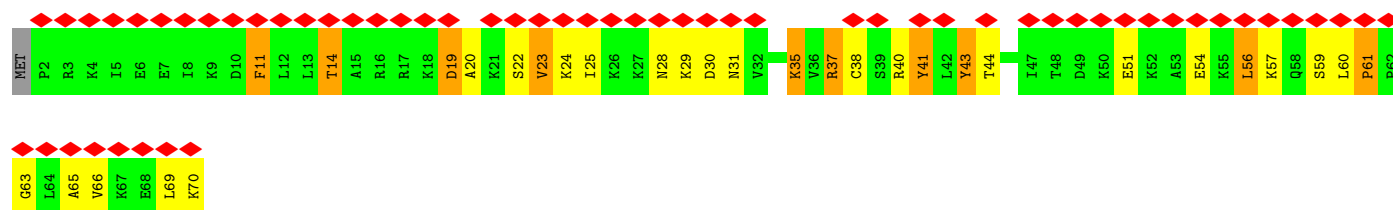
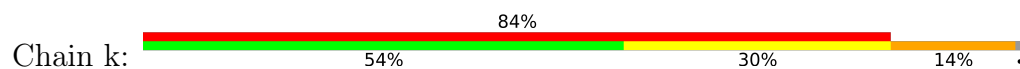


• Molecule 38: Ribosomal protein eL37

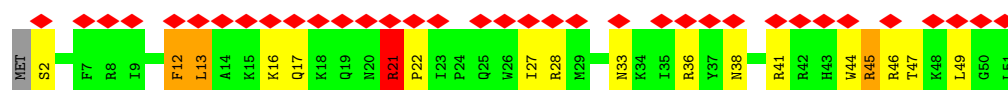




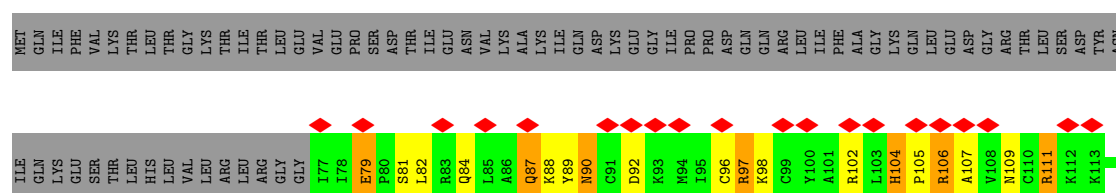
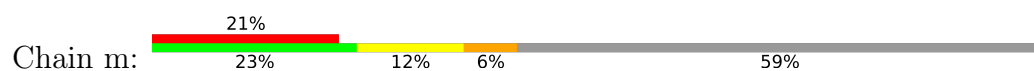
• Molecule 39: Ribosomal protein eL38



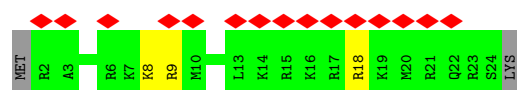
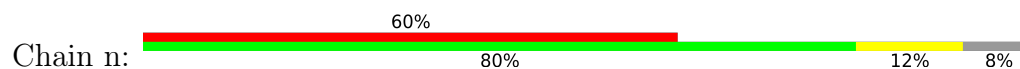
• Molecule 40: Ribosomal protein eL39



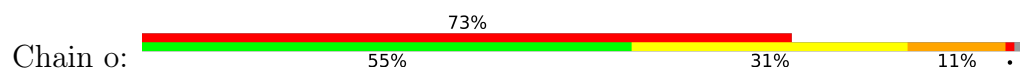
• Molecule 41: Ribosomal protein eL40



• Molecule 42: Ribosomal protein eL41

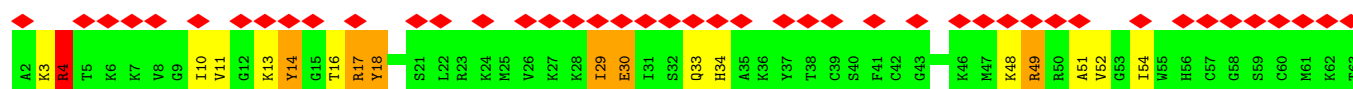
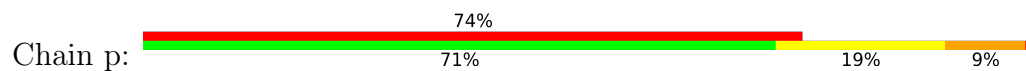


• Molecule 43: Ribosomal protein eL42

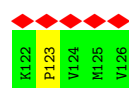
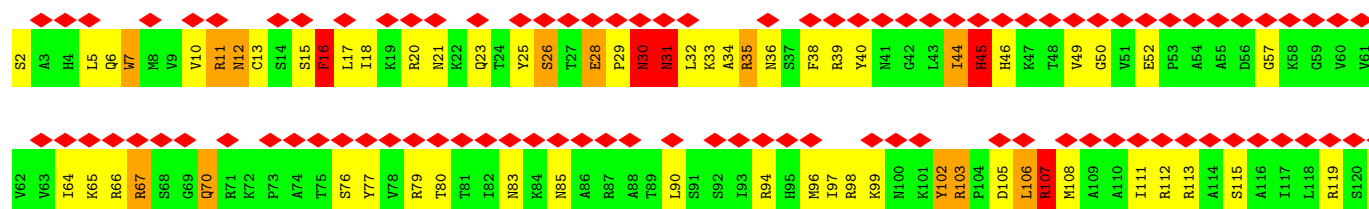
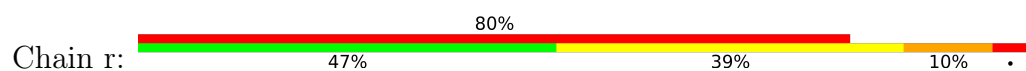




• Molecule 44: Ribosomal protein eL43



• Molecule 45: Ribosomal protein eL28



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	80019	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.933	Depositor
Minimum map value	-0.562	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.065	Depositor
Map size ($\text{\AA}$)	549.4, 549.4, 549.4	wwPDB
Map dimensions	410, 410, 410	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	5	0.59	23/87792 (0.0%)	1.26	1288/136945 (0.9%)
2	7	0.51	1/2858 (0.0%)	1.11	16/4455 (0.4%)
3	8	0.62	0/3701	1.30	64/5766 (1.1%)
4	A	1.06	8/1906 (0.4%)	1.40	32/2556 (1.3%)
5	B	1.02	11/3214 (0.3%)	1.30	32/4308 (0.7%)
6	C	0.95	3/2973 (0.1%)	1.24	19/3990 (0.5%)
7	D	0.95	9/2426 (0.4%)	1.39	30/3252 (0.9%)
8	E	0.99	7/1941 (0.4%)	1.39	19/2601 (0.7%)
9	F	1.03	2/1905 (0.1%)	1.51	36/2539 (1.4%)
10	G	0.90	4/1966 (0.2%)	1.25	14/2645 (0.5%)
11	H	0.90	2/1537 (0.1%)	1.29	11/2066 (0.5%)
12	I	0.84	2/1753 (0.1%)	1.28	21/2343 (0.9%)
13	J	0.76	1/1382 (0.1%)	1.10	8/1849 (0.4%)
14	L	0.93	3/1734 (0.2%)	1.26	15/2318 (0.6%)
15	M	0.92	2/1152 (0.2%)	1.27	12/1539 (0.8%)
16	N	1.01	5/1746 (0.3%)	1.49	30/2338 (1.3%)
17	O	0.93	2/1684 (0.1%)	1.30	14/2251 (0.6%)
18	P	0.96	1/1268 (0.1%)	1.21	8/1701 (0.5%)
19	Q	0.89	1/1530 (0.1%)	1.41	24/2041 (1.2%)
20	R	0.97	7/1524 (0.5%)	1.42	22/2013 (1.1%)
21	S	1.20	8/1493 (0.5%)	1.45	28/2002 (1.4%)
22	T	0.88	1/1326 (0.1%)	1.21	12/1770 (0.7%)
23	U	0.83	3/822 (0.4%)	1.12	4/1103 (0.4%)
24	V	1.08	5/993 (0.5%)	1.26	6/1332 (0.5%)
25	W	0.91	1/541 (0.2%)	1.28	0/720
26	X	0.85	3/993 (0.3%)	1.26	7/1334 (0.5%)
27	Y	0.94	3/1132 (0.3%)	1.32	15/1504 (1.0%)
28	Z	0.84	0/1130	1.21	6/1507 (0.4%)
29	a	1.20	7/1192 (0.6%)	1.57	20/1591 (1.3%)
30	b	0.99	3/620 (0.5%)	1.45	11/819 (1.3%)
31	c	0.94	3/742 (0.4%)	1.31	9/996 (0.9%)
32	d	1.08	6/903 (0.7%)	1.46	14/1216 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	1.05	5/1071 (0.5%)	1.39	20/1429 (1.4%)
34	f	1.15	4/895 (0.4%)	1.37	16/1198 (1.3%)
35	g	0.87	0/916	1.22	8/1220 (0.7%)
36	h	0.82	1/1023 (0.1%)	1.26	9/1350 (0.7%)
37	i	0.85	2/843 (0.2%)	1.29	8/1115 (0.7%)
38	j	1.13	4/721 (0.6%)	1.57	16/953 (1.7%)
39	k	0.74	1/575 (0.2%)	1.15	3/761 (0.4%)
40	l	0.85	0/454	1.25	6/599 (1.0%)
41	m	0.77	0/435	1.14	1/575 (0.2%)
42	n	0.63	0/223	1.10	0/284
43	o	0.83	1/864 (0.1%)	1.34	8/1140 (0.7%)
44	p	0.80	0/718	1.22	7/953 (0.7%)
45	r	0.89	1/1017 (0.1%)	1.31	13/1365 (1.0%)
All	All	0.74	156/147634 (0.1%)	1.28	1962/218352 (0.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	5	1	155
2	7	0	2
3	8	0	11
4	A	0	6
5	B	0	13
6	C	0	5
7	D	0	8
8	E	0	12
9	F	0	5
10	G	0	3
11	H	0	3
12	I	0	5
13	J	0	2
14	L	0	5
15	M	0	4
16	N	0	11
17	O	0	3
18	P	0	1
19	Q	0	5
20	R	0	6
21	S	0	11

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Mol	Chain	#Chirality outliers	#Planarity outliers
22	T	0	2
23	U	0	2
24	V	0	3
25	W	0	1
26	X	0	1
27	Y	0	4
29	a	0	9
30	b	0	1
31	c	0	2
32	d	0	4
33	e	0	4
34	f	0	2
35	g	0	1
36	h	0	3
37	i	0	3
38	j	0	4
39	k	0	1
43	o	0	6
44	p	0	1
45	r	0	5
All	All	1	335

The worst 5 of 156 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1823	G	O3'-P	33.20	2.10	1.61
21	S	81	TRP	CA-CB	14.98	1.71	1.53
29	a	109	TYR	CA-CB	14.18	1.72	1.53
8	E	278	TYR	CA-CB	14.00	1.72	1.53
24	V	97	TYR	CA-CB	12.45	1.73	1.53

The worst 5 of 1962 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	E	278	TYR	CB-CA-C	21.49	129.78	110.44
17	O	135	PHE	N-CA-C	17.86	134.68	108.60
11	H	156	ASN	N-CA-C	-17.44	92.41	111.07
3	8	34	U	C4'-C3'-O3'	-16.90	87.66	113.00
1	5	383	A	C1'-C2'-O2'	-15.04	89.25	111.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	5	1992	U	C1'

5 of 335 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	5	22	G	Sidechain
1	5	31	U	Sidechain
1	5	42	A	Sidechain
1	5	43	U	Sidechain
1	5	53	C	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5	78486	0	39661	10404	0
2	7	2558	0	1296	305	0
3	8	3314	0	1683	507	0
4	A	1868	0	1959	163	0
5	B	3147	0	3280	227	0
6	C	2919	0	3100	175	0
7	D	2380	0	2412	182	0
8	E	1904	0	2055	148	0
9	F	1870	0	1996	179	0
10	G	1934	0	2086	106	0
11	H	1518	0	1601	85	0
12	I	1713	0	1752	90	0
13	J	1359	0	1390	61	0
14	L	1703	0	1818	104	0
15	M	1131	0	1209	77	0
16	N	1701	0	1749	128	0
17	O	1651	0	1786	90	0
18	P	1242	0	1269	57	0
19	Q	1506	0	1623	78	0
20	R	1508	0	1664	91	0
21	S	1454	0	1496	124	0
22	T	1298	0	1366	83	0
23	U	808	0	831	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	V	979	0	1039	52	0
25	W	528	0	541	52	0
26	X	976	0	1053	38	0
27	Y	1115	0	1205	65	0
28	Z	1107	0	1182	56	0
29	a	1163	0	1211	107	0
30	b	610	0	650	49	0
31	c	732	0	769	41	0
32	d	888	0	930	63	0
33	e	1053	0	1147	91	0
34	f	876	0	912	58	0
35	g	906	0	1002	56	0
36	h	1015	0	1149	56	0
37	i	832	0	917	29	0
38	j	706	0	743	52	0
39	k	569	0	637	21	0
40	l	444	0	483	13	0
41	m	429	0	466	26	0
42	n	222	0	264	0	0
43	o	851	0	922	44	0
44	p	708	0	760	26	0
45	r	1001	0	1062	75	0
46	5	119	0	0	0	0
46	7	5	0	0	0	0
46	8	4	0	0	0	0
46	P	1	0	0	0	0
46	V	1	0	0	0	0
47	j	1	0	0	1	0
47	m	1	0	0	0	0
47	o	1	0	0	1	0
All	All	136815	0	98126	13356	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 57.

The worst 5 of 13356 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:100:C:C5	1:5:101:A:C8	2.00	1.49
1:5:1266:G:N2	1:5:2111:G:N3	1.67	1.41
1:5:1174:G:N2	1:5:1175:A:N7	1.67	1.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2361:G:O6	18:P:25:HIS:CD2	1.74	1.38
1:5:4283:G:C2	1:5:4284:C:C6	2.13	1.37

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A	242/257 (94%)	203 (84%)	30 (12%)	9 (4%)	2	16
5	B	392/394 (100%)	319 (81%)	40 (10%)	33 (8%)	0	4
6	C	365/367 (100%)	304 (83%)	46 (13%)	15 (4%)	2	15
7	D	290/297 (98%)	235 (81%)	33 (11%)	22 (8%)	1	5
8	E	232/236 (98%)	150 (65%)	51 (22%)	31 (13%)	0	1
9	F	223/225 (99%)	190 (85%)	23 (10%)	10 (4%)	2	12
10	G	239/266 (90%)	200 (84%)	32 (13%)	7 (3%)	3	19
11	H	188/192 (98%)	164 (87%)	20 (11%)	4 (2%)	5	24
12	I	211/213 (99%)	168 (80%)	30 (14%)	13 (6%)	1	7
13	J	168/178 (94%)	137 (82%)	23 (14%)	8 (5%)	2	11
14	L	208/211 (99%)	172 (83%)	25 (12%)	11 (5%)	1	10
15	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	8	30
16	N	201/204 (98%)	172 (86%)	23 (11%)	6 (3%)	3	18
17	O	199/204 (98%)	182 (92%)	14 (7%)	3 (2%)	8	30
18	P	151/153 (99%)	140 (93%)	9 (6%)	2 (1%)	9	33
19	Q	185/188 (98%)	160 (86%)	20 (11%)	5 (3%)	4	20
20	R	178/196 (91%)	153 (86%)	21 (12%)	4 (2%)	5	24
21	S	173/224 (77%)	146 (84%)	24 (14%)	3 (2%)	7	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	T	157/160 (98%)	128 (82%)	26 (17%)	3 (2%)	6	26
23	U	97/128 (76%)	74 (76%)	21 (22%)	2 (2%)	5	24
24	V	129/140 (92%)	112 (87%)	14 (11%)	3 (2%)	5	23
25	W	61/157 (39%)	57 (93%)	3 (5%)	1 (2%)	7	29
26	X	117/156 (75%)	108 (92%)	7 (6%)	2 (2%)	7	28
27	Y	132/145 (91%)	112 (85%)	14 (11%)	6 (4%)	2	12
28	Z	133/136 (98%)	113 (85%)	16 (12%)	4 (3%)	3	18
29	a	145/148 (98%)	111 (77%)	26 (18%)	8 (6%)	1	9
30	b	73/160 (46%)	58 (80%)	11 (15%)	4 (6%)	1	9
31	c	92/115 (80%)	78 (85%)	10 (11%)	4 (4%)	2	13
32	d	105/125 (84%)	85 (81%)	16 (15%)	4 (4%)	2	15
33	e	126/135 (93%)	110 (87%)	15 (12%)	1 (1%)	16	44
34	f	107/110 (97%)	95 (89%)	7 (6%)	5 (5%)	2	12
35	g	112/117 (96%)	103 (92%)	7 (6%)	2 (2%)	6	26
36	h	120/123 (98%)	103 (86%)	14 (12%)	3 (2%)	4	21
37	i	100/105 (95%)	91 (91%)	7 (7%)	2 (2%)	6	25
38	j	84/86 (98%)	67 (80%)	13 (16%)	4 (5%)	2	11
39	k	67/70 (96%)	55 (82%)	7 (10%)	5 (8%)	1	5
40	l	48/51 (94%)	42 (88%)	4 (8%)	2 (4%)	2	14
41	m	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
42	n	21/25 (84%)	21 (100%)	0	0	100	100
43	o	102/106 (96%)	85 (83%)	11 (11%)	6 (6%)	1	8
44	p	89/91 (98%)	79 (89%)	9 (10%)	1 (1%)	11	38
45	r	123/125 (98%)	97 (79%)	20 (16%)	6 (5%)	1	11
All	All	6371/7060 (90%)	5341 (84%)	764 (12%)	266 (4%)	3	14

5 of 266 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	19	HIS
4	A	197	PRO
5	B	16	PHE
5	B	40	PRO
5	B	108	GLU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	187/199 (94%)	141 (75%)	46 (25%)	1	2
5	B	335/335 (100%)	267 (80%)	68 (20%)	1	4
6	C	305/305 (100%)	242 (79%)	63 (21%)	1	4
7	D	246/250 (98%)	179 (73%)	67 (27%)	0	1
8	E	209/209 (100%)	162 (78%)	47 (22%)	1	3
9	F	194/194 (100%)	143 (74%)	51 (26%)	0	1
10	G	206/226 (91%)	156 (76%)	50 (24%)	1	2
11	H	169/171 (99%)	126 (75%)	43 (25%)	0	1
12	I	180/180 (100%)	140 (78%)	40 (22%)	1	3
13	J	143/149 (96%)	111 (78%)	32 (22%)	1	3
14	L	176/177 (99%)	135 (77%)	41 (23%)	1	2
15	M	116/160 (72%)	95 (82%)	21 (18%)	2	7
16	N	171/172 (99%)	132 (77%)	39 (23%)	1	3
17	O	172/174 (99%)	144 (84%)	28 (16%)	2	10
18	P	134/134 (100%)	113 (84%)	21 (16%)	2	10
19	Q	163/164 (99%)	132 (81%)	31 (19%)	1	6
20	R	159/175 (91%)	119 (75%)	40 (25%)	0	1
21	S	156/192 (81%)	121 (78%)	35 (22%)	1	3
22	T	139/140 (99%)	117 (84%)	22 (16%)	2	10
23	U	89/114 (78%)	70 (79%)	19 (21%)	1	3
24	V	101/107 (94%)	79 (78%)	22 (22%)	1	3
25	W	55/126 (44%)	42 (76%)	13 (24%)	1	2
26	X	107/133 (80%)	87 (81%)	20 (19%)	1	6
27	Y	124/135 (92%)	92 (74%)	32 (26%)	0	1
28	Z	117/118 (99%)	94 (80%)	23 (20%)	1	5
29	a	119/120 (99%)	104 (87%)	15 (13%)	4	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	b	63/123 (51%)	46 (73%)	17 (27%)	0	1
31	c	79/97 (81%)	61 (77%)	18 (23%)	1	3
32	d	98/110 (89%)	66 (67%)	32 (33%)	0	0
33	e	114/121 (94%)	87 (76%)	27 (24%)	1	2
34	f	88/89 (99%)	69 (78%)	19 (22%)	1	3
35	g	98/100 (98%)	80 (82%)	18 (18%)	1	7
36	h	109/110 (99%)	91 (84%)	18 (16%)	2	10
37	i	86/89 (97%)	69 (80%)	17 (20%)	1	5
38	j	73/73 (100%)	61 (84%)	12 (16%)	2	10
39	k	64/65 (98%)	54 (84%)	10 (16%)	2	10
40	l	47/48 (98%)	39 (83%)	8 (17%)	2	9
41	m	48/116 (41%)	35 (73%)	13 (27%)	0	1
42	n	22/24 (92%)	19 (86%)	3 (14%)	3	15
43	o	92/94 (98%)	71 (77%)	21 (23%)	1	3
44	p	74/74 (100%)	62 (84%)	12 (16%)	2	10
45	r	109/109 (100%)	92 (84%)	17 (16%)	2	10
All	All	5536/6001 (92%)	4345 (78%)	1191 (22%)	3	3

5 of 1191 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	a	85	GLN
43	o	33	LEU
31	c	56	ARG
29	a	77	LYS
34	f	103	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 187 such sidechains are listed below:

Mol	Chain	Res	Type
21	S	50	GLN
29	a	62	HIS
21	S	163	HIS
26	X	93	ASN
31	c	40	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3652/3664 (99%)	1667 (45%)	629 (17%)
2	7	119/120 (99%)	31 (26%)	9 (7%)
3	8	155/156 (99%)	61 (39%)	22 (14%)
All	All	3926/3940 (99%)	1759 (44%)	660 (16%)

5 of 1759 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	5	A
1	5	6	C
1	5	8	U
1	5	12	A

5 of 660 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	3860	A
1	5	4645	C
1	5	4084	G
1	5	3856	A
1	5	4287	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 133 ligands modelled in this entry, 133 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	13
8	E	1

The worst 5 of 14 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	72:ALA	C	84:VAL	N	23.51
1	5	4776:G	O3'	4859:C	P	17.87
1	5	757:G	O3'	906:C	P	16.89
1	5	519:C	O3'	642:G	P	16.61
1	5	2910:G	O3'	3583:U	P	16.04

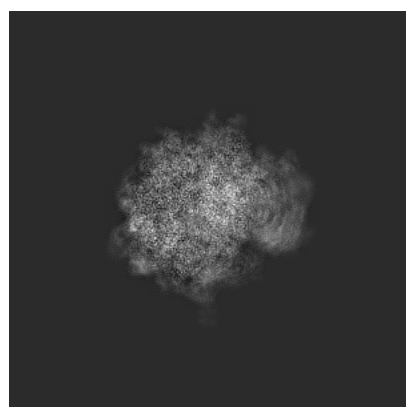
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2649. These allow visual inspection of the internal detail of the map and identification of artifacts.

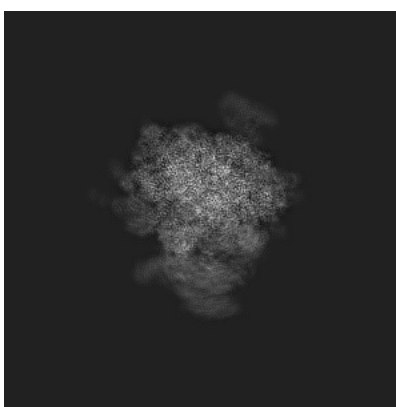
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

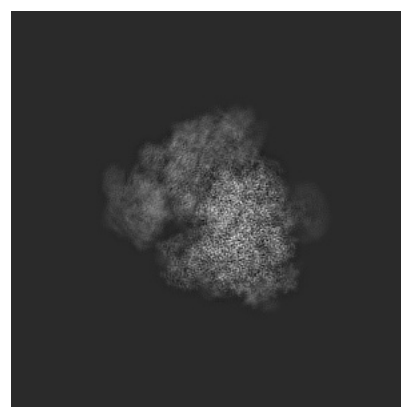
6.1.1 Primary map



X



Y

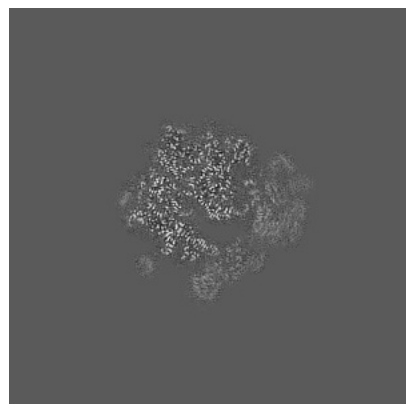


Z

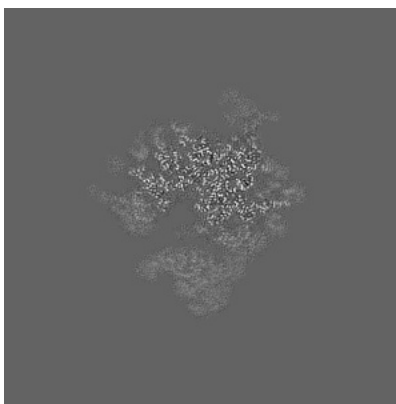
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

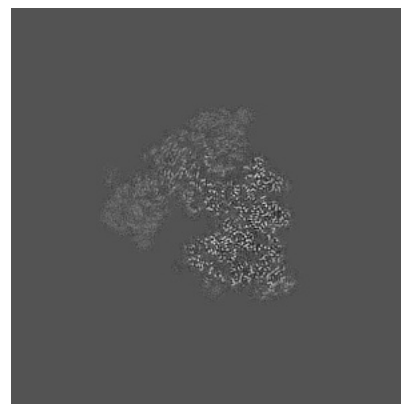
6.2.1 Primary map



X Index: 205



Y Index: 205

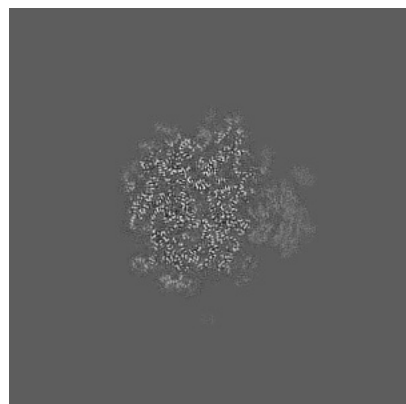


Z Index: 205

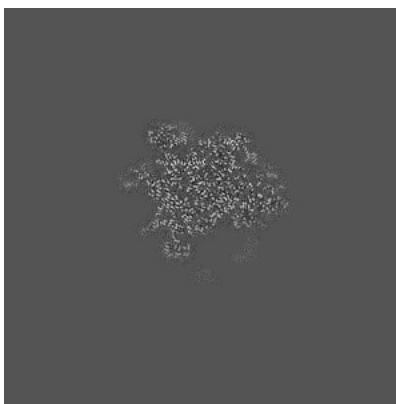
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

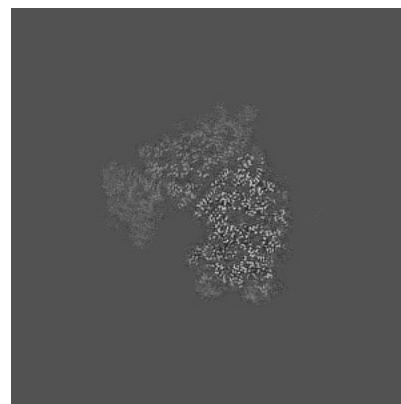
6.3.1 Primary map



X Index: 228



Y Index: 162

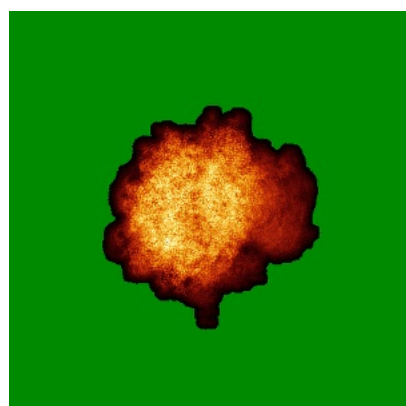


Z Index: 216

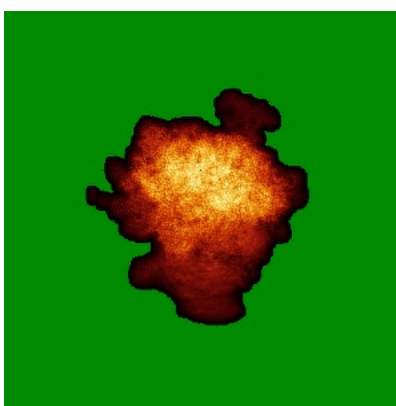
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

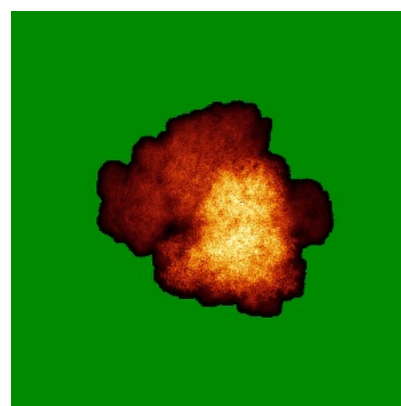
6.4.1 Primary map



X



Y

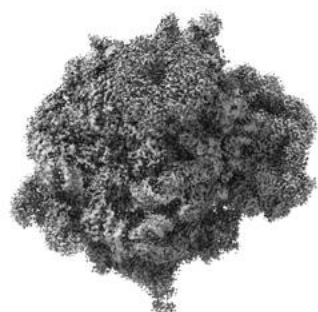


Z

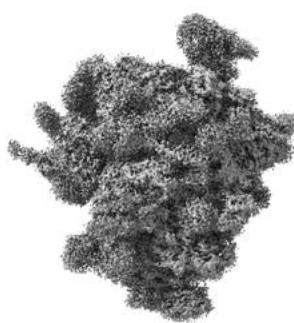
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

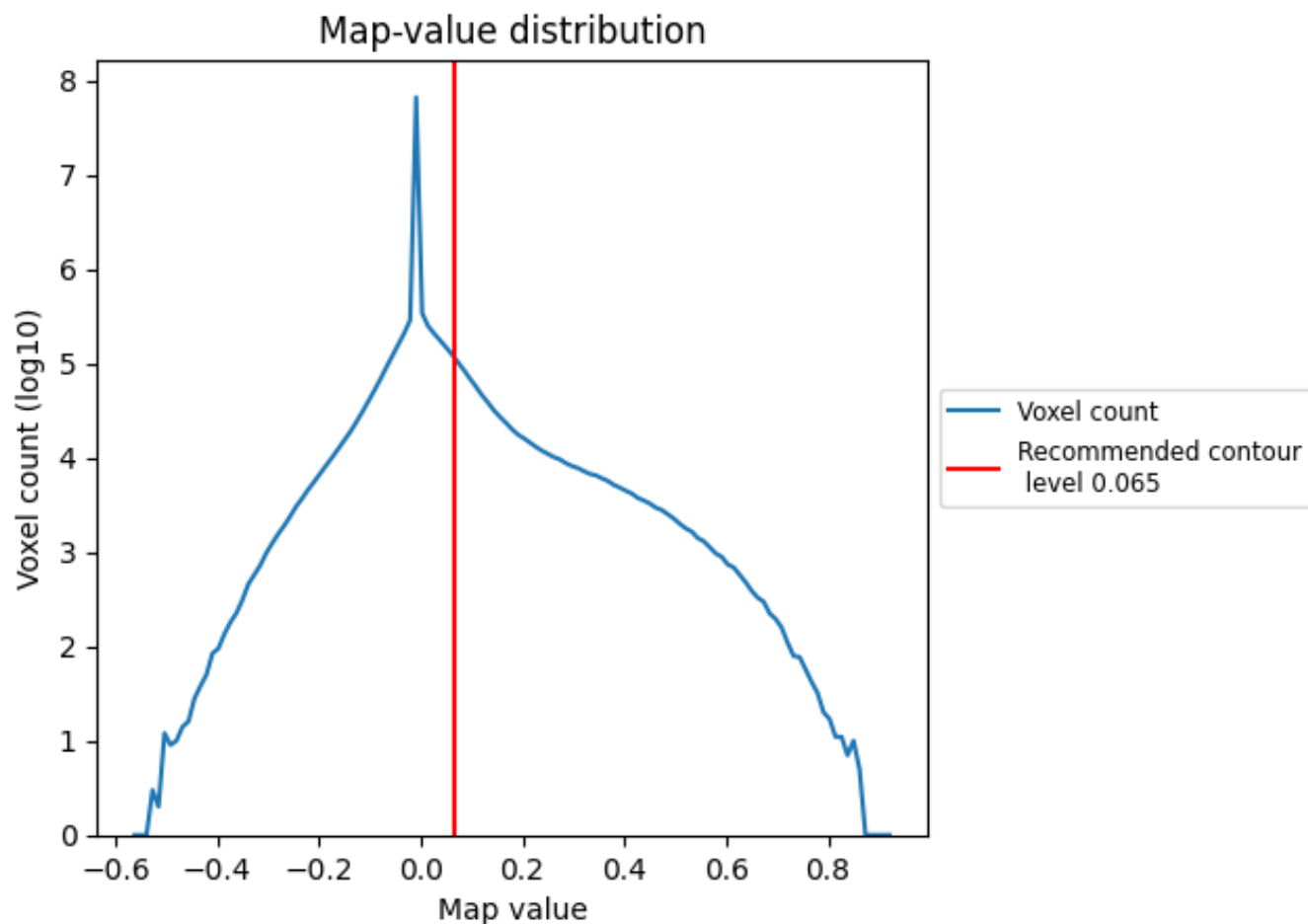
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

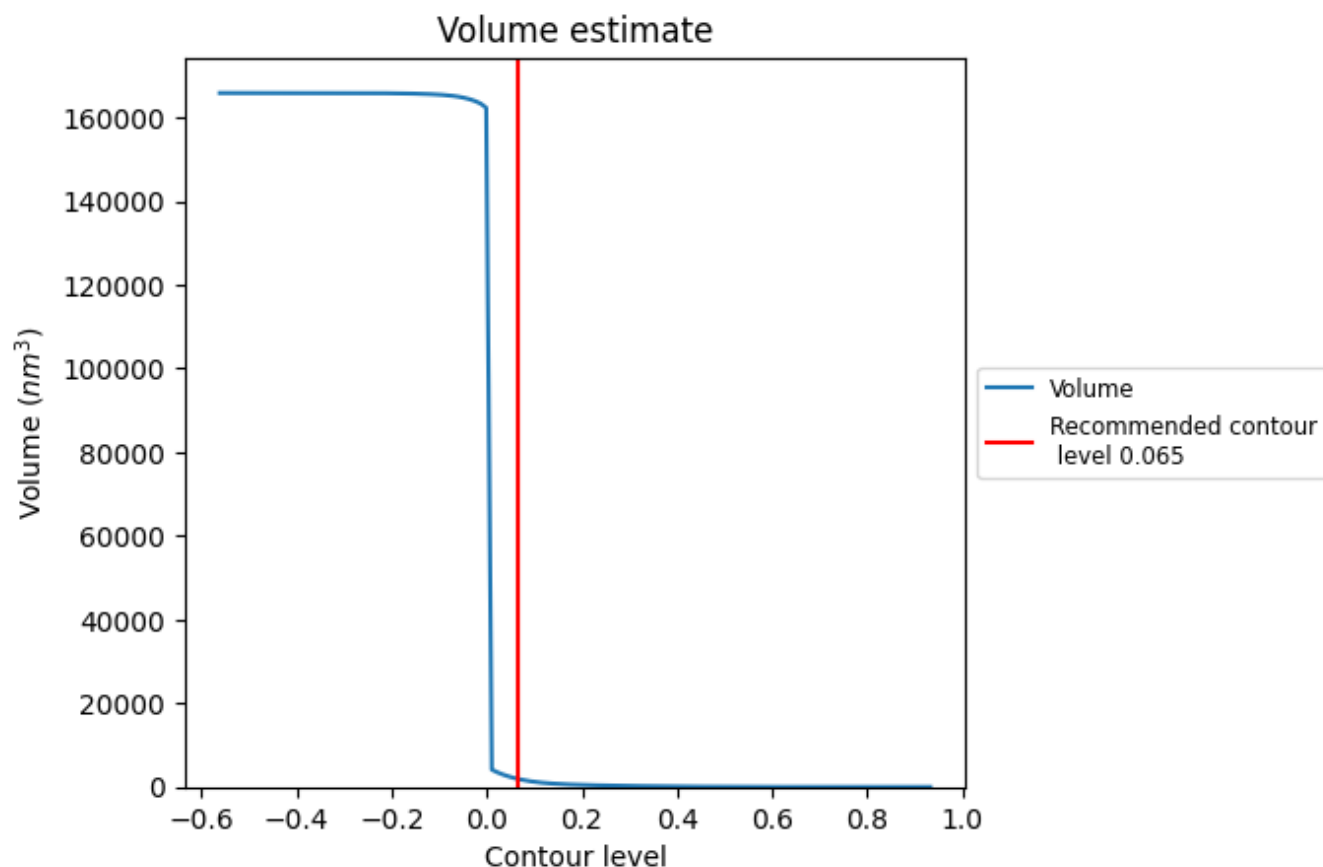
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

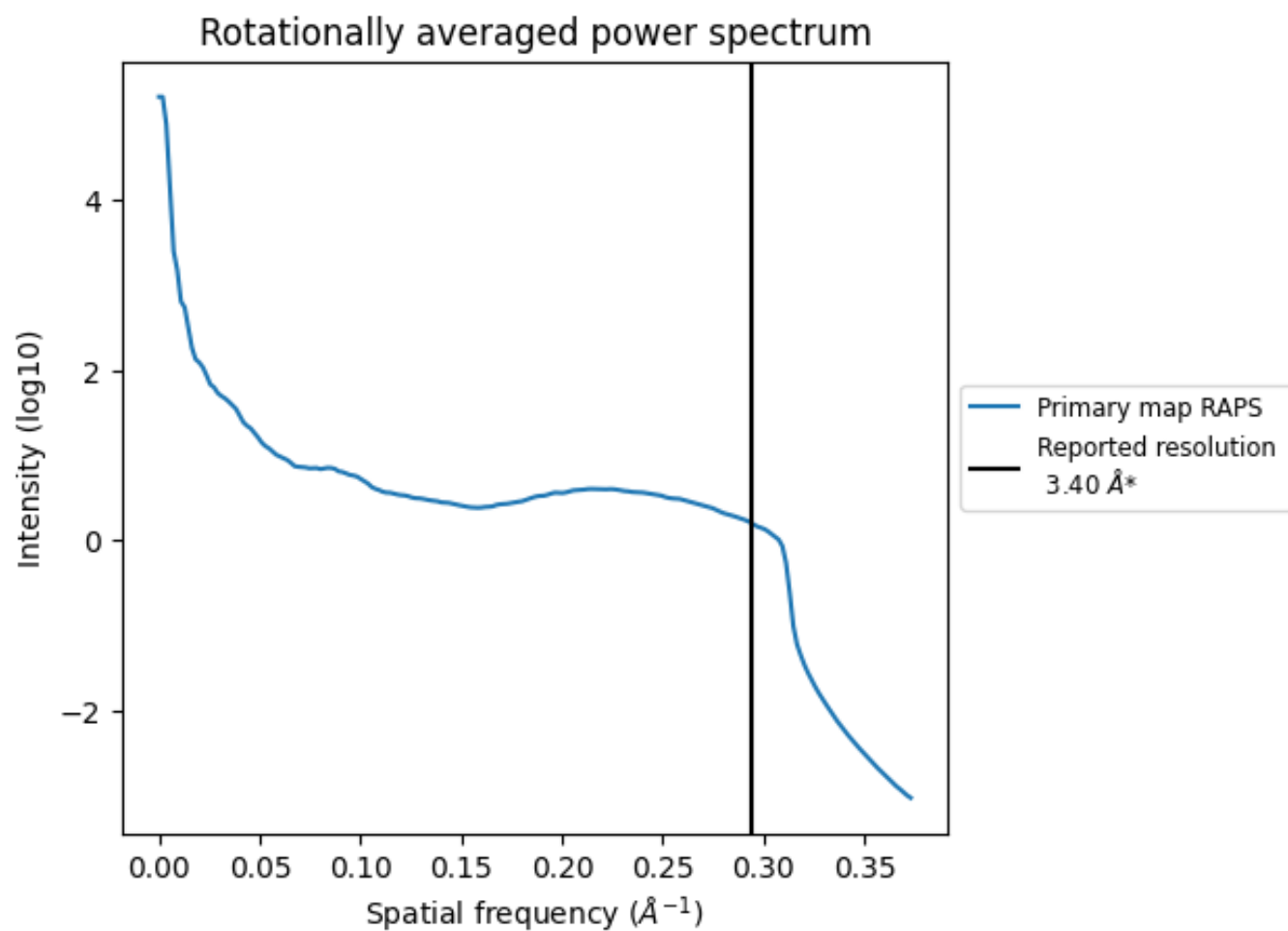
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1930 nm³; this corresponds to an approximate mass of 1743 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

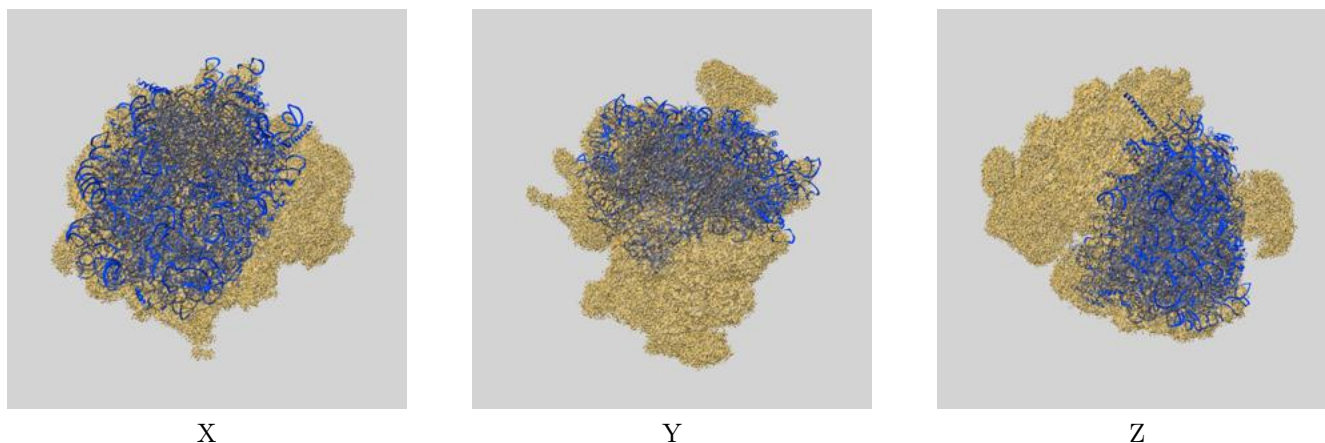
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

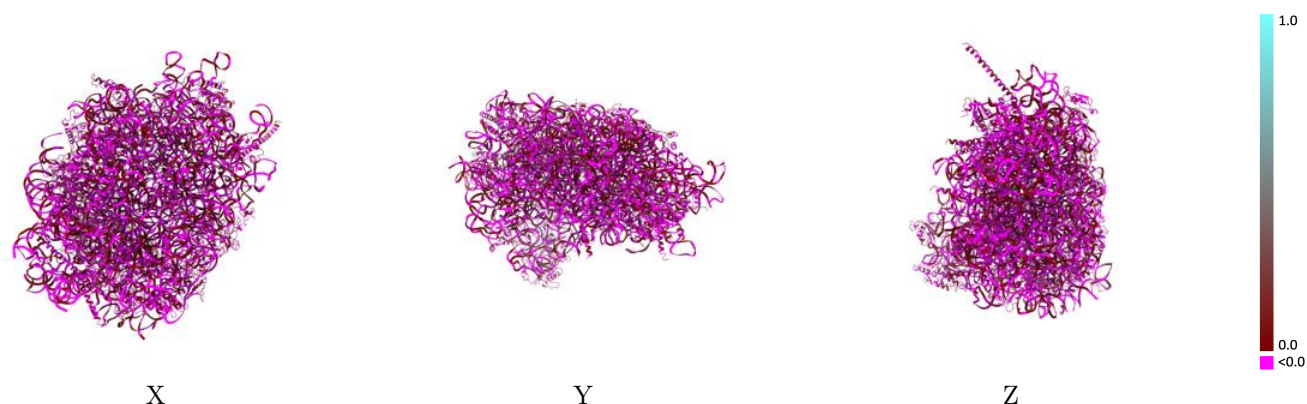
This section contains information regarding the fit between EMDB map EMD-2649 and PDB model 3J7O. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



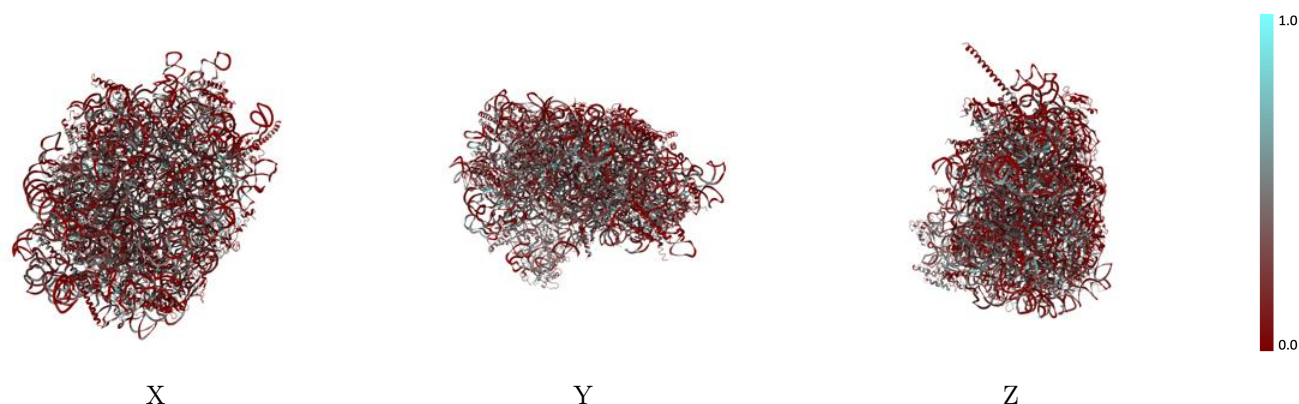
The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



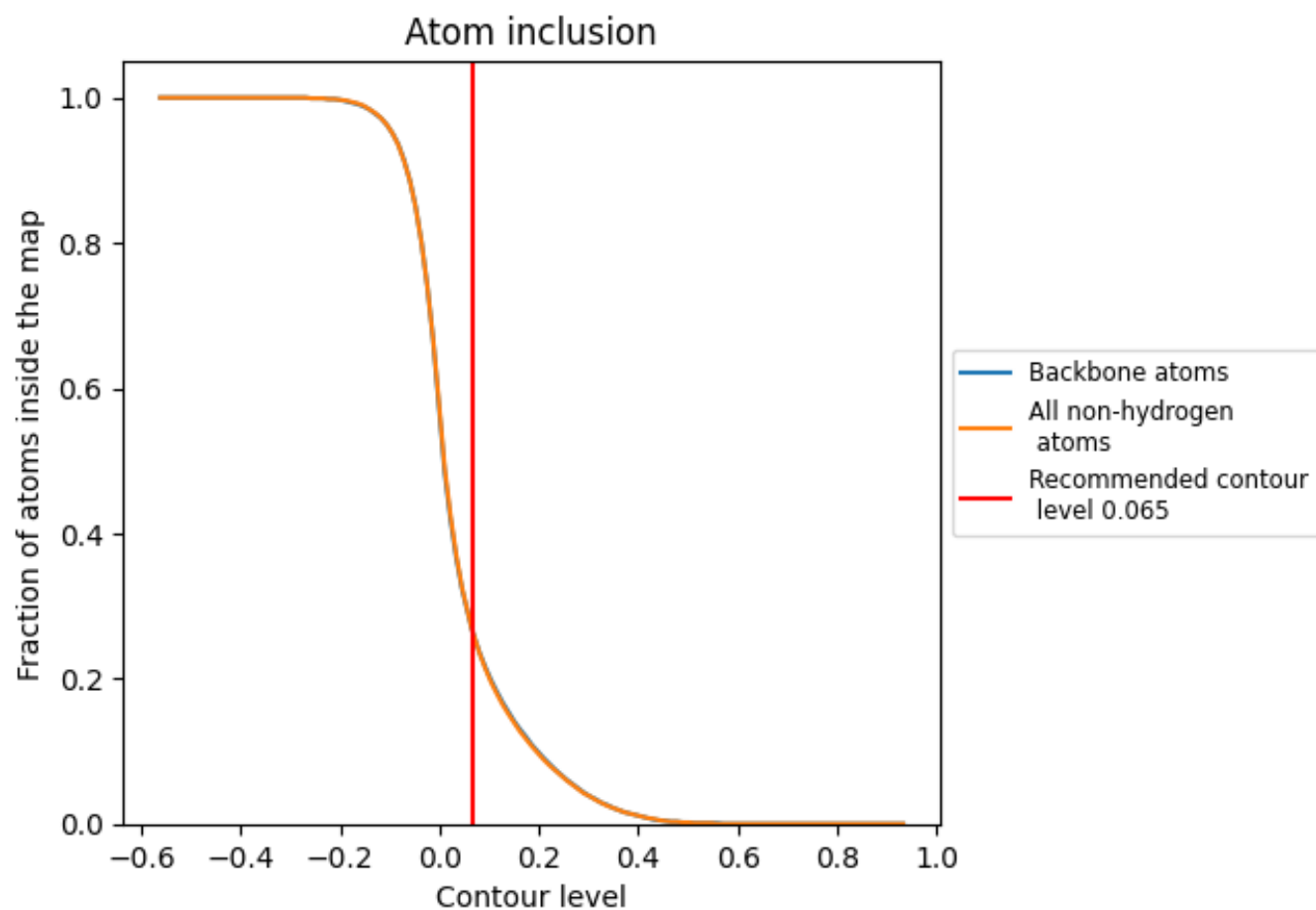
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.065).

9.4 Atom inclusion [i](#)



At the recommended contour level, 27% of all backbone atoms, 27% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2680	 -0.0180
5	 0.2710	 -0.0170
7	 0.3270	 -0.0110
8	 0.2350	 -0.0150
A	 0.3340	 -0.0290
B	 0.2520	 -0.0310
C	 0.3020	 -0.0240
D	 0.3080	 -0.0100
E	 0.2670	 -0.0330
F	 0.2950	 -0.0510
G	 0.2280	 -0.0110
H	 0.1740	 -0.0300
I	 0.3030	 -0.0230
J	 0.2820	 -0.0140
L	 0.2410	 -0.0100
M	 0.2610	 -0.0370
N	 0.3020	 -0.0090
O	 0.2630	 -0.0130
P	 0.2390	 -0.0130
Q	 0.3200	 -0.0230
R	 0.2100	 -0.0030
S	 0.3370	 -0.0150
T	 0.3170	 -0.0300
U	 0.1290	 -0.0120
V	 0.2640	 -0.0050
W	 0.2460	 -0.0290
X	 0.1520	 -0.0110
Y	 0.1590	 -0.0050
Z	 0.2090	 -0.0260
a	 0.3360	 -0.0120
b	 0.2070	 -0.0440
c	 0.2450	 -0.0010
d	 0.1380	 -0.0100
e	 0.2590	 -0.0370
f	 0.3140	 -0.0170



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Chain	Atom inclusion	Q-score
g	 0.3230	 -0.0210
h	 0.1840	 0.0010
i	 0.3150	 -0.0090
j	 0.3070	 -0.0070
k	 0.1180	 -0.0100
l	 0.2950	 -0.0110
m	 0.3890	 -0.0320
n	 0.2980	 -0.0330
o	 0.2410	 -0.0050
p	 0.2330	 -0.0090
r	 0.2130	 -0.0170